

110682

Schreiber, David

From: Ramirez, Delia
Sent: Wednesday, December 17, 2003 10:38 AM
To: Schreiber, David
Subject: case 09/879792

Hi,

I would like to order the following interference search: seq id 11 and 12 in the nucleic acid databases.

Thank you,

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Patent Examiner
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	1	1748	100.0	1748	9	US-09-879-732-11	Sequence 11, Appl
	2	1670.4	95.6	2393	13	US-10-333-690-99	Sequence 99, Appl
	3	1429	81.8	1614	9	US-09-888-615-45	Sequence 15, Appl
	4	1302.8	74.5	1314	11	US-09-898-837A-14	Sequence 14, Appl
C	5	1302.8	74.5	1314	11	US-09-898-837A-17	Sequence 17, Appl
	6	1258.6	72.0	1434	15	US-10-177-661-1	Sequence 1, Appl
C	7	1068.4	61.1	1078	11	US-09-898-837A-16	Sequence 16, Appl
	8	1062.6	60.8	1341	15	US-10-177-661-3	Sequence 3, Appl
	9	1053	60.2	1230	9	US-09-879-732-35	Sequence 35, Appl
	10	782.4	44.8	1222	9	US-09-804-156-5	Sequence 5, Appl
	11	782.4	44.8	1222	10	US-09-946-633-3	Sequence 3, Appl
	12	782.4	44.8	1222	13	US-10-319-519-5	Sequence 5, Appl
	13	782.4	44.8	1222	14	US-10-125-459-3	Sequence 3, Appl
	14	782.4	44.8	1222	14	US-10-067-761-5	Sequence 5, Appl
	15	709.4	40.6	834	9	US-09-879-732-28	Sequence 28, Appl

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Db 61 TCGAGCATCTCCAGCCCAAGGCATCTCCAGCTGGGACACCTCCAGGCGCGGCATCTCCAGC 120
Qy 121 CCAGGCATCTCCAGCCCAAGGCATCTCCAGCTGGGACACCTCCAGGCGCGGCATCTCCAGC 180
Db 121 CCAGGCATCTCCAGCCCAAGGCATCTCCAGCTGGGACACCTCCAGGCGCGGCATCTCCAGC 180
Qy 181 CCAGGCATCTCCAGCTGGTCACTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGC 240
Db 181 CCAGGCATCTCCAGCTGGTCACTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGC 240
Qy 241 CCAGGCATCTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGC 300
Db 241 CCAGGCATCTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGC 300
Qy 301 CAGGTCATCATCCGCCAGGCTCAGGCTCGGTCGAGCTGAGGCTGAGGCTGAGGCTGAGGCTG 360
Db 301 CAGGTCATCATCCGCCAGGCTCAGGCTCGGTCGAGCTGAGGCTGAGGCTGAGGCTGAGGCTG 360
Qy 361 TAGAGCAACCAAGTGGGCTGTACCCATCCGATCATCTCCAGGCTGAGGCTGAGGCTGAGGCTG 420
Db 361 TAGAGCAACCAAGTGGGCTGTACCCATCCGATCATCTCCAGGCTGAGGCTGAGGCTGAGGCTG 420
Qy 421 AACAGGGCCACCAAGGAGGAGCCAGGTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
Db 421 AACAGGGCCACCAAGGAGGAGCCAGGTACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
Qy 481 CCAGAGCAGCTACCGCTCATCCGGTGGCTGCTCTCTCATTCGCTGCTGCTGCTGCTGCTGCT 540
Db 481 CCAGAGCAGCTACCGCTCATCCGGTGGCTGCTCTCTCATTCGCTGCTGCTGCTGCTGCTGCT 540
Qy 541 CATCATCTCTTCAGTCTTGGCAGGGCCACAGGATCAGGATCAGGATCAGGATCAGGATCAGG 600
Db 541 CATCATCTCTTCAGTCTTGGCAGGGCCACAGGATCAGGATCAGGATCAGGATCAGGATCAGG 600
Qy 601 GAGCTGTCCCAAGCAGCTGTCTGTGAGCGGGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 660
Db 601 GAGCTGTCCCAAGCAGCTGTCTGTGAGCGGGTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 660
Qy 661 CGAGCTGGGCTGGTGGAGTTTGA CTGGGCAAGTCTCTGCTTAAATCTACTCTGGGTC 720
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Qy 721 CTCCATCAGTGGCTTCCATCTGTAGCAGCACTGGAATGATCTCTACTCAGAGAGAC 780
Db 721 CTCCATCAGTGGCTTCCATCTGTAGCAGCACTGGAATGATCTCTACTCAGAGAGAC 780
Qy 781 CTGCCAGCAGCTGGGTTTCGAGAGTGTCTACCGGACAAACGAGGTTGCCACAGGATTT 840
Db 781 CTGCCAGCAGCTGGGTTTCGAGAGTGTCTACCGGACAAACGAGGTTGCCACAGGATTT 840
Qy 841 TGCCAAACAGCTTCTCAATCTTGAGATCAACTCCACCATCCAGGAAAGCTTCCACAGGTC 900
Db 841 TGCCAAACAGCTTCTCAATCTTGAGATCAACTCCACCATCCAGGAAAGCTTCCACAGGTC 900
Qy 901 TGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCACCTGCGGACTGAGGGCCAT 960
Db 901 TGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCACCTGCGGACTGAGGGCCAT 960
Qy 961 GACCGGCGGATCTGGGAGGGGCGCTGGCTCGGATAGCAAGTGGCTTGGCAAGTGAG 1020
Db 961 GACCGGCGGATCTGGGAGGGGCGCTGGCTCGGATAGCAAGTGGCTTGGCAAGTGAG 1020
Qy 1021 TCTGCACTTGGGACCAACCACTCTGTGGAGGCAACGCTCATTCAGCCCAAGTGGGTC 1080
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Qy 1081 CACTGCGGCCACTGCTTCTCTGAGCCCGGAGAGGCTCTGAGGCGCTGGAAGTGTA 1140
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Qy 1141 CGCGGGCACCAAGCAACCTGACCAAGTGGCTTGGGAGGAGGCTTCCATTTGCCGAGATCATCAT 1200
Db 1141 CGCGGGCACCAAGCAACCTGACCAAGTGGCTTGGGAGGAGGCTTCCATTTGCCGAGATCATCAT 1200

Qy 1201 CAAACGCAATTACACCGATGAGGAGGACGACTATATGACATCGCCCTCATTCGGGCTGTCCAA 1260
Db 1201 CAAACGCAATTACACCGATGAGGAGGACGACTATATGACATCGCCCTCATTCGGGCTGTCCAA 1260
Qy 1261 GCGGCTGACGCTGTTCGCTCAGATCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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Qy 1321 TAGGCTCAATGAGACCTGCTGCTGATCAGAGCTTTGGCAAGCAGGAGGAGAGAGATGACAA 1380
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Qy 1381 GACATCCCCCTTCTCCGAGGAGTGCAGGTCATCTCATCTGATCTTCAAGAAATGCAATGA 1440
Db 1381 GACATCCCCCTTCTCCGAGGAGTGCAGGTCATCTCATCTGATCTTCAAGAAATGCAATGA 1440
Qy 1441 CTACTTGGTCTATGACAGTTTACCTTACCCCAAGGATGATGTGCTGGGACCTTCTGGG 1500
Db 1441 CTACTTGGTCTATGACAGTTTACCTTACCCCAAGGATGATGTGCTGGGACCTTCTGGG 1500
Qy 1501 GGGCAGAGACTCTCTGCGAGGAGGAGCAGCGGGGGGCTCTTGTCTGTGAGCAGAACCG 1560
Db 1501 GGGCAGAGACTCTCTGCGAGGAGGAGCAGCGGGGGGCTCTTGTCTGTGAGCAGAACCG 1560
Qy 1561 CTGGTACTGTCAGGCTGTACAGCTGGGGGCA CAGGCTGTGGGCAAGAAACCAACCTGG 1620
Db 1561 CTGGTACTGTCAGGCTGTACAGCTGGGGGCA CAGGCTGTGGGCAAGAAACCAACCTGG 1620
Qy 1621 TGTGTACACCAAAAGTGACAGAGTTCTTCCCTGATTTACAGCAAGATGAGAGCGAGGT 1680
Db 1621 TGTGTACACCAAAAGTGACAGAGTTCTTCCCTGATTTACAGCAAGATGAGAGCGAGGT 1680
Qy 1681 GCGATTCAGAAAATCTTAACAGCTGGCTGTCTGCTGACAGCAGCAGGCTGTCTGTGAC 1740
Db 1681 GCGATTCAGAAAATCTTAACAGCTGGCTGTCTGCTGACAGCAGCAGGCTGTCTGTGAC 1740
Qy 1741 TCGAGAAA 1748
Db 1741 TCGAGAAA 1748

RESULT 2

US-10-353-690-99

; Sequence 99, Application US/10353690

; Publication No. US20030215840A1

; GENERAL INFORMATION:

; APPLICANT: Logan, Thomas Joseph

; APPLICANT: Chun, Miyoung

; APPLICANT: Galvin, Katherine M.

; APPLICANT: Healy, Aileen

; APPLICANT: Acton, Susan L.

; APPLICANT: Donoghue, Mary

; APPLICANT: Stagliano, Nancy

; APPLICANT: Perodin, Jaquelin

; APPLICANT: Rodrigue-Way, Amelie

; TITLE OF INVENTION: Methods and compositions for treating

; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,

; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,

; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,

; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,

; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,

; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2314,

; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,

; FILE REFERENCE: MPI02-018PIENOMNIN

; CURRENT APPLICATION NUMBER: US/10/353,690

; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 60/353,224

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/364,529

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: 60/373,861

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; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-99

Query Match      95.6%; Score 1670.4; DB 13; Length 2393;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCAGAGACATCGAGAGGACAGCCAGCGGATGATCTCCAGCAAGAACACCTTCAGC 60
DB 78 CTCAGAGACATCGAGAGGACAGCCAGCGGATGATCTCCAGCAAGAACACCTTCAGC 137
QY 61 TGGAGCATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 120
DB 138 TGGAGCATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 197
QY 121 CAGGACATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 180
DB 198 CAGGACATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 257
QY 181 CAGGACATCTCCAGCTGGGTACACCTCCAGGCGGGCACTCTCCAGGCGGGCATCTCCAGC 240
DB 258 CAGGACATCTCCAGCTGGGTACACCTCCAGGCGGGCACTCTCCAGGCGGGCATCTCCAGC 317
QY 241 CAGGACATCTCCAGGCGGGCACTCTCCAGCTGGGACACCTTCAGGTCCTCATCCG 300
DB 318 CAGGACATCTCCAGGCGGGCACTCTCCAGCTGGGACACCTTCAGGTCCTCATCCG 377
QY 301 CAGGTCATCATCCGCGAGGTCCAGCTCCGCTGGTACAACTCCCAACAGAGGTGTACCTTGT 360
DB 378 CAGGTCATCATCCGCGAGGTCCAGCTCCGCTGGTACAACTCCCAACAGAGGTGTACCTTGT 437
QY 361 TAGAGCAACACAGTGGGGGCTGTACCCATCCGATCATCTCTCCAGGCTCAGCACAGC 420
DB 438 TAGAGCAACACAGTGGGGGCTGTACCCATCCGATCATCTCTCCAGGCTCAGCACAGC 497
QY 421 AACAGGGCCACAGGGAGGCGGATAGAGGTACAGGCTCCGCAAGTTCACTTGGGGAGGG 480
DB 498 AACAGGGCCACAGGGAGGCGGATAGAGGTACAGGCTCCGCAAGTTCACTTGGGGAGGG 557
QY 481 CCAGAGCAGGTACCGCTCATCCGGGTGCTGCTCCCTCATTTGCTCCCTGGTGGTTCGCT 540
DB 558 CCAGAGCAGGTACCGCTCATCCGGGTGCTGCTCCCTCATTTGCTCCCTGGTGGTTCGCT 617
QY 541 CATCATCTCTTCCAGTCTTGGCAGGGCCACACAGGGATCAGGTACAGGAGCAGAGGGA 600
DB 618 CATCATCTCTTCCAGTCTTGGCAGGGCCACACAGGGATCAGGTACAGGAGCAGAGGGA 677
QY 601 GAGCTGTCCAGACAGCTGTGCTGTGACGGGGTGGTGGATCGAAGCTGAAGAGTGA 660
DB 678 GAGCTGTCCAGACAGCTGTGCTGTGACGGGGTGGTGGATCGAAGCTGAAGAGTGA 737
QY 661 CGAGCTGGGCTGGCTGAGGTTTGACTGGGACAGTCTCTGCTTAAATCTACTCTGGGTC 720
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DB 738 CGAGCTGGGCTGGCTGAGGTTTGACTGGGCAAGTCTCTGCTTAAATCTACTCTGGGTC 797
QY 721 CTCCTCATCAGTGGCTTCCCATCTGTAGCAGCACTTGGAAATGATCTCTACTCAGAGAGAC 780
DB 798 CTCCTCATCAGTGGCTTCCCATCTGTAGCAGCACTTGGAAATGATCTCTACTCAGAGAGAC 857
QY 781 CTGCCAGCAGCTGGGTTTCGAGAGTCTCAACGGACACCGAGGTTGCCCAAGAGATTT 840
DB 858 CTGCCAGCAGCTGGGTTTCGAGAGTCTCAACGGACACCGAGGTTGCCCAAGAGATTT 917
QY 841 TGCCCAACAGCTTCTCAATCTTCAGATACAACTCCACCATCCAGGAAGCTCCACAGGTC 900
DB 918 TGCCCAACAGCTTCTCAATCTTCAGATACAACTCCACCATCCAGGAAGCTCCACAGGTC 977
QY 901 TGAATGCCCTTCCCAAGCGGTATATCTCTCCCTCCAGTGTTCCTCCAGCTGAGGGCCAT 960
DB 978 TGAATGCCCTTCCCAAGCGGTATATCTCTCCCTCCAGTGTTCCTCCAGCTGAGGGCCAT 1037
QY 961 GACCGGGCGGATCTGGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCCCTTGGCAAGTGAG 1020
DB 1038 GACCGGGCGGATCTGGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCCCTTGGCAAGTGAG 1097
QY 1021 TCTGCACTTCCGCAACCCACCATCTGTGGAGGCACTCTCATTTGACGCGGCTGGTGTCT 1080
DB 1098 TCTGCACTTCCGCAACCCACCATCTGTGGAGGCACTCTCATTTGACGCGGCTGGTGTCT 1157
QY 1081 CACTGCGGCCACTGTCTTCTGTGACCCGGGAGAGGTCCTGGAGGGCTTGGAGGTGTA 1140
DB 1158 CACTGCGGCCACTGTCTTCTGTGACCCGGGAGAGGTCCTGGAGGGCTTGGAGGTGTA 1217
QY 1141 CCGGGCAACCAAGAACTGCAACAGTTGCTTGGAGGAGCTCCATTTGCCAGATCATCAT 1200
DB 1218 CCGGGCAACCAAGAACTGCAACAGTTGCTTGGAGGAGCTCCATTTGCCAGATCATCAT 1277
QY 1201 CACAGCAATTTACCCGATGAGGAGGAGCACTATGACATGCGCTCATTCGGCTGTCCAA 1260
DB 1278 CACAGCAATTTACCCGATGAGGAGGAGCACTATGACATGCGCTCATTCGGCTGTCCAA 1337
QY 1261 GCGCTTGACCTGTGCTGCTCAGATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1338 GCGCTTGACCTGTGCTGCTCAGATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1397
QY 1321 TAGCTTCAATAGAGCTGCTGGATCAGAGCTTTGGCAAGACAGGGAGACAGATGACAA 1380
DB 1398 TAGCTTCAATAGAGCTGCTGGATCAGAGCTTTGGCAAGACAGGGAGACAGATGACAA 1457
QY 1381 GACATCCCTTCCCTCCGGAGGTGAGGTCAATCTCATGCACTTCAGAAATGCAATGA 1440
DB 1458 GACATCCCTTCCCTCCGGAGGTGAGGTCAATCTCATGCACTTCAGAAATGCAATGA 1517
QY 1441 CTACTTGGTCTATGACAGTTTACCTTACCCCAAGGATGATGTGCTGGGAGCTTGGTGG 1500
DB 1518 CTACTTGGTCTATGACAGTTTACCTTACCCCAAGGATGATGTGCTGGGAGCTTGGTGG 1577
QY 1501 GGGCAGAGACTCTCTGCGCAGGGAGACAGCGGGGGGCTCTTGTCTGTGAGCAAGAACCG 1560
DB 1578 GGGCAGAGACTCTCTGCGCAGGGAGACAGCGGGGGGCTCTTGTCTGTGAGCAAGAACCG 1637
QY 1561 CTGTGTACCTGGCAGGTGTGACAGGCTGGGGGCAAGGCTGTGGCCAGAGAACTGG 1620
DB 1638 CTGTGTACCTGGCAGGTGTGACAGGCTGGGGGCAAGGCTGTGGCCAGAGAACTGG 1697
QY 1621 TGTGTACCAAGTGAAGAGTGTCTTCTCTGGATTTTACAGCAAGATGGAG 1672
DB 1698 TGTGTACCAAGTGAAGAGTGTCTTCTCTGGATTTTACAGCAAGATGGAG 1749
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RESULT 3
US-09-888-615-45
; Sequence 45, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:

APPLICANT:	FLOWMAN, GREGORY	APPLICANT:	WHITE, DAVID	APPLICANT:	CAENEPEEL, SEAN	APPLICANT:	CHARYDCZAK, GLEN	APPLICANT:	MANNING, GERARD	APPLICANT:	SUDARSANAM, SUCHA	TITLE OF INVENTION:	NOVEL PROTEASES	FILE REFERENCE:	038602/1214	CURRENT APPLICATION NUMBER:	US/09/888,615	PRIOR FILING DATE:	2001-06-26	PRIOR FILING DATE:	2000-06-26	NUMBER OF SEQ ID NOS:	150	SOFTWARE:	PatentIn Ver. 2.1	SEQ ID NO	45	LENGTH:	1614	TYPE:	DNA	ORGANISM:	Homo sapiens	US-09-888-615-45	
Query Match	81.8%	Score	1429	DB	9	Length	1614	Best Local Similarity	92.1%	Pred	No	0	Matches	1584	Conservative	0	Mismatches	0	Indels	135	Gaps	2													
QY	11	ATGAGAGGACGAGCAGCGGAATGCAATCTCCAGCAAGAACCTTTCAGCTGGAGCATCT	70																																
DB	1	ATGAGAGGACGAGCAGCGGAATGCAATCTCCAGCAAGAACCTTTCAGCTGGAGCATCT	60																																
QY	71	CCAGCCAGGCATCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	130																																
DB	61	CCAGCCAGGCATCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	120																																
QY	131	CCAGCCAGGCATCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	190																																
DB	121	CCAGCCAGGCATCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	180																																
QY	191	CCAGCTGGTACACCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	228																																
DB	181	CCAGCTGGTACACCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	240																																
QY	229	-----GGCATCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	280																																
DB	241	CCAGGCCAGGCATCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	300																																
QY	281	CTTTCAGGCTCTCCATCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	340																																
DB	301	CTTTCAGGCTCTCCATCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	360																																
QY	341	CCAGCCAGGCATCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	400																																
DB	361	CCAGCCAGGCATCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	420																																
QY	401	CTTTCAGGCTCTCCATCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGGCCAGGCATCT	460																																
DB	421	CTTTCAGGCTCTCCATCCAGGCGGG																																	

; NUMBER OF SEQ ID NOS: 53									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 16									
; LENGTH: 1078									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-898-837A-16									
Query Match									
Best Local Similarity 61.1%; Score 1068.4; DB 11; Length 1078;									
Matches 1069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	670	CTGCGTGGAGTTTGACTGGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTCTCCCATCA	729						
DB	1078	CTGCGTGGAGTTTGACTGGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTCTCCCATCA	1019						
QY	730	GTGGCTTCCATCTGTAGAGCAACTGGAAATGATCTCTACTCAGAGAAGACCTGCCAGCA	789						
DB	1018	GTGGCTTCCATCTGTAGAGCAACTGGAAATGATCTCTACTCAGAGAAGACCTGCCAGCA	959						
QY	790	GCTGGGTTTCGAGAGTGCTCACCGGACAAACCGAGTTGCCACAGGGATTTTCCCAACAG	849						
DB	958	GCTGGGTTTCGAGAGTGCTCACCGGACAAACCGAGTTGCCACAGGGATTTTCCCAACAG	899						
QY	850	CTTCTCAATCTTGAGATACAACTCCACCATCCAGGAAAGCTCCACAGGFTCTGAATGCC	909						
DB	898	CTTCTCAATCTTGAGATACAACTCCACCATCCAGGAAAGCTCCACAGGFTCTGAATGCC	839						
QY	910	TTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTGAGGCCATGACCGGGCG	969						
DB	838	TTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTGAGGCCATGACCGGGCG	779						
QY	970	GATCGTGGGAGGGCGCTGGCTCGGATAGCAAGTGCCCTTGGCAAGTGTCTGCACTT	1029						
DB	778	GATCGTGGGAGGGCGCTGGCTCGGATAGCAAGTGTGGCTTGGCAAGTGTCTGCACTT	719						
QY	1030	CGGCACACCCACATCTGTGTGAGGACACGCTCATTTGACGCCAGCGGTGTCTACCTGCCG	1089						
DB	718	CGGCACACCCACATCTGTGTGAGGACACGCTCATTTGAGGCCAGGTGGTGTCTACCTGCCG	659						
QY	1090	CCACTGCTTCTTGAGACCCGGGAGAGGTCTCTGGAGGGCTGGAGGTGTACGGGGCAC	1149						
DB	658	CCACTGCTTCTTGAGACCCGGGAGAGGTCTCTGGAGGGCTGGAGGTGTACGGGGCAC	599						
QY	1150	CAGCAACTGACACAGTTGCTCTGAGGACAGCTCCATTTGCCAGATCATCATCAACAGCAA	1209						
DB	598	CAGCAACTGACACAGTTGCTCTGAGGACAGCTCCATTTGCCAGATCATCATCAACAGCAA	539						
QY	1210	TTACACCGATGAGGAGACGACTATGACATCGCCCTCATGCGGCTGTCCAAAGCCCTGAC	1269						
DB	538	TTACACCGATGAGGAGACGACTATGACATCGCCCTCATGCGGCTGTCCAAAGCCCTGAC	479						
QY	1270	CCTGTCCGCTCACATCCACCTGCTTGCTCCCATGATGACAGACCTTTAGCTCAA	1329						
DB	478	CCTGTCCGCTCACATCCACCTGCTTGCTCCCATGATGACAGACCTTTAGCTCAA	419						
QY	1330	TGAGACCTGCTGGATCAACAGGCTTTGGCAAGACCAAGGAGACAGATGACAAACATCCCC	1389						
DB	418	TGAGACCTGCTGGATCAACAGGCTTTGGCAAGACCAAGGAGACAGATGACAAACATCCCC	359						
QY	1390	CTTCTCCGGAGGTGAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGT	1449						
DB	358	CTTCTCCGGAGGTGAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGT	299						
QY	1450	CTATGACAGTTTACCTTACCCCAAGATGATGTGCTGGGACCTTCTGGGGGACAGAGA	1509						
DB	298	CTATGACAGTTTACCTTACCCCAAGATGATGTGCTGGGACCTTCTGGGGGACAGAGA	239						
QY	1510	CTCTGCCAGGAGACAGCGGGGGGCTCTTGTGTGTGAGCAGAAACAAACCGCTGGTACCT	1569						
DB	238	CTCTGCCAGGAGACAGCGGGGGGCTCTTGTGTGTGAGCAGAAACAAACCGCTGGTACCT	179						
QY	1570	GGCAGGTGTACCAGCTGGGGGACAGGCTGTGGCCAGAGAAACAAACCTGGTGTATAC	1629						

DB	178	GGCAGGTGTACCAGCTGGGGGACAGGCTGTGGCCAGAGAAACAAACCTGGTGTATAC	119						
QY	1630	CAAAGTGACAGAGTTCTTCCCTCGATTTCACGCAAGATGAGAGCGAGTTCGATTTCAG	1689						
DB	118	CAAAGTGACAGAGTTCTTCCCTCGATTTCACGCAAGATGAGAGCGAGTTCGATTTCAC	59						
QY	1690	AAAAATCCTAACCAAGCTGGCTCTCTCTGCAAGCACCGGCTGTGTGA	1739						
DB	58	AAAAATCCTAACCAAGCTGGCTCTCTCTGCAAGCACCGGCTGTGTGA	9						

RESULT 8

US-10-177-661-3

; Sequence 3, Application US/10177661

; Publication No. US20030082783A1

GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Virca, G. Duke

; TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE

; FILE REFERENCE: 3256-A

; CURRENT APPLICATION NUMBER: US/10/177,661

; CURRENT FILING DATE: 2002-06-20

; PRIOR APPLICATION NUMBER: US 60/299,606

; PRIOR FILING DATE: 2001-06-20

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1341

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1341)

; OTHER INFORMATION:

US-10-177-661-3

Query Match

Best Local Similarity 60.8%; Score 1062.6; DB 15; Length 1341;

Matches 1177; Conservative 0; Mismatches 19; Indels 93; Gaps 1;

QY	411	CAGCACAGCAACCCAGGGCCACAGGAGAGCCAGCTAGAGCTGCCAAGTTCACT	470						
DB	146	CAGCCTCATATTCCTCCCTGCTGCCGCCCTGTCTTAGTAGAGCTGCCAAGTTCACT	205						
QY	471	GGCGGAGGGCCAGAGCAGCTACCGCTCATCGGGTGGTGTCTCTCTCATTTGCCCTGG	530						
DB	206	GGCGGAGGGCCAGAGCAGCTACCGCTCATCGGGTGGTGTCTCTCTCATTTGCCCTGG	265						
QY	531	TGGTTTCGCTCATCTCTTCCAGTTCTGGCAGGGCCACACAGGGATCAGGTACAGG	590						
DB	266	TGGTTTCGCTCATCTCTTCCAGTTCTGGCAGGGCCACACAGGGATCAGGTACAGG	325						
QY	591	AGCAGAGGAGAGCTGTCCTCAAGCAGCTGTTCCTGTGACGGGTGGTGTGACCTGCAAGC	650						
DB	326	AGCAGAGGAGAGCTGTCCTCAAGCAGCTGTTCCTGTGACGGGTGGTGTGACCTGCAAGC	385						
QY	651	TGAAGAGTGACGAGCTGGGCTGGTGTGAGTTTGACTGCGACAGTCTCTCTTAAATCT	710						
DB	386	TGAAGAGTGACGAGCTGGGCTGGTGTGAGTTTGACTGCGACAGTCTCTCTTAAATCT	445						
QY	711	ACTTGGGTCTCCCATCAGTGGCTTCCATCTGTAGCAGCACTGGATGACTCTTACT	770						
DB	446	ACTTGGGTCTCCCATCAGTGGCTTCCATCTGTAGCAGCACTGGATGACTCTTACT	505						
QY	771	CAGAGAGAGCTGCCAGCAGCTGGGTTTCGAGAGTGTCTCACCGGACACGAGGTGGCC	830						
DB	506	CAGAGAGAGCTGCCAGCAGCTGGGTTTCGAGAGTGTCTCACCGGACACGAGGTGGCC	537						
QY	831	ACAGGGATTTTGCCCAACAGCTTCTCAATCTTGAAGATACAACTCCACCATCAGGAAAGCC	890						
DB	538	-----	537						

QY 891 TCACAGAGTCTGAATGCGCTTCCAGCGGTATATCTCCCTCCAGTGTTCACATCGCGAC 950
Db 538 -----AGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCACATCGCGAC 592
QY 951 TGAGGGCCATGACCGGGCGATCGTGGAGGGCGCTGGCTCGATAGCAAGTGGCCTT 1010
Db 593 TGAGGGCCATGACCGGGCGATCGTGGAGGGCGCTGGCTCGATAGCAAGTGGCCTT 652
QY 1011 GGCAAGTGAAGTCTGCACTTCGGGACCAACCCACATCTGTGGAGGACGCTCATTTGACGCC 1070
Db 653 GGCAAGTGAAGTCTGCACTTCGGGACCAACCCACATCTGTGGAGGACGCTCATTTGACGCC 712
QY 1071 AGTGGGTGCTCACTGCGGCCCATCTGCTTCTGTGACCCCGGAGAGGCTCTGGAGGCT 1130
Db 713 AGTGGGTGCTCACTGCGGCCCATCTGCTTCTGTGACCCCGGAGAGGCTCTGGAGGCT 772
QY 1131 GGAAGGTGACGGGGGACAGCAACCTGACCAAGTTGCTGAGGACGCTCCATTGCCG 1190
Db 773 GGAAGGTGACGGGGGACAGCAACCTGACCAAGTTGCTGAGGACGCTCCATTGCCG 832
QY 1191 AGATCATCATCAACAGCAATTTACACCGATGAGGAGGACGATATGACATCGCCCTCATGC 1250
Db 833 AGATCATCATCAACAGCAATTTACACCGATGAGGAGGACGATATGACATCGCCCTCATGC 892
QY 1251 GGCTGTCCAGCCCTGACCCCTGCTCCGCTCATCTCCACCTGCTGCTCCCATGCAATG 1310
Db 893 GGCTGTCCAGCCCTGACCCCTGCTCCGCTCATCTCCACCTGCTGCTCCCATGCAATG 952
QY 1311 GACAGACCTTTAGGCTCAATGAGACCTGCTGGATCAAGGCTTTGGCAAGACCAAGGAGA 1370
Db 953 GACAGACCTTTAGGCTCAATGAGACCTGCTGGATCAAGGCTTTGGCAAGACCAAGGAGA 1012
QY 1371 CAGATGACAGACATCCCTTCTCCGAGAGTGTGAGGTCATCTCATGACATTCAGAA 1430
Db 1013 CAGATGACAGACATCCCTTCTCCGAGAGTGTGAGGTCATCTCATGACATTCAGAA 1072
QY 1431 AATCGATGACATCTGCTATGACAGTTACCTTACCCAGGATGATGCTGCTGGG 1490
Db 1073 AATCGATGACATCTGCTATGACAGTTACCTTACCCAGGATGATGCTGCTGGG 1132
QY 1491 ACCTTCGTGGGGGACAGACTCTCCGACAGGAGACAGCGGGGGCTCTTCTGTGTGAGC 1550
Db 1133 ACCTTCGTGGGGGACAGACTCTCCGACAGGAGACAGCGGGGGCTCTTGTGTGTGAGC 1192
QY 1551 AGAACAAACCGCTGTGATCTGACAGGTGTACAGCTGGGGGACAGGCTGTGGGACAGAA 1610
Db 1193 AGAACAAACCGCTGTGATCTGACAGGTGTACAGCTGGGGGACAGGCTGTGGGACAGAA 1252
QY 1611 ACAACCTGTGTGTACACCAAGTGTACAGAGTTCTTCCCTGATTTTACAGCAAGATGG 1670
Db 1253 ACAACCTGTGTGTGTACACCAAGTGTACAGAGTTCTTCCCTGATTTTACAGCAAGATGG 1312
QY 1671 AGAGCGAGGTGCGATTTCAGAAATCTCTAA 1699
Db 1313 AGAGCGAGGTGCGATTTCAGAAATCTCTAA 1341

RESULT 9

US-09-879-792-35

; Sequence 35, Application US/09879792

; Patent No. US20020061850A1

; GENERAL INFORMATION:

; APPLICANT: Xiao, Yonhong

; APPLICANT: Gedrich, Richard

; TITLE OF INVENTION: Regulation of Human Transmembrane Serine

; TITLE OF INVENTION: Protease

; FILE REFERENCE: 02973.00035

; CURRENT APPLICATION NUMBER: US/09/879,792

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/211,224

; PRIOR FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: US 60/283,353

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/283,648
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT _____ (Docket No. US20020061850A1 LIO-81-WO)
; PRIOR FILING DATE: 2001-06-12

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 1230

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(1230)

; OTHER INFORMATION: n = A, T, C or G

US-09-879-792-35

Query Match 60.2%; Score 1053; DB 9; Length 1230;

Best Local Similarity 92.1%; Pred. No. 1.3e-291;

Matches 1134; Conservative 0; Mismatches 84; Indels 13; Gaps 2;

QY 521 ATTGCCCTGTGTGTTTCGCTCATCATCTCTTCAGTTCTGGGAGGGGCAACAGGGATC 580

Db 1 ATGACCCAGCTGTCTGCTTCTTTTCTCTAGTCCAGTTCTGGCAGNNCCACACAGNNATC 60

QY 581 AGGTACAGGAGCAGAGGAGAGCTGTCCAGCAGCTGTCCGCTGTGACGGGGTGTG 640

Db 61 AGGTACAGGAGCAGAGGAGAGCTGTCCAGCAGCTGTCCGCTGTGACGGGGTGTG 120

QY 641 GACTGCAAGCTGAAGAGTGAAGCTGGGCTGGCTGTGAGGTTTGTGCTGGGACAACTCTG 700

Db 121 GACTGCAAGCTGAAGAGTGAAGCTGGGCTGGCTGTGAGGTTTGTGCTGGGACAACTCTG 180

QY 701 CTTAAAAATCTACTCTGGGTCTCTCCATCACTGAGTGTTCCTCATCTGTAGCAGCAACTGGAAT 760

Db 181 CTTAAAAATCTACTCTGGGTCTCTCCATCACTGAGTGTTCCTCATCTGTAGCAGCAACTGGAAT 240

QY 761 GACTCCTACTCTGAGAGAGCTGTCCAGCAGCTGTGGTTTCCAGAGTGTCTCCGAGCAACC 820

Db 241 GACTCCTACTCTGAGAGAGCTGTCCAGCAGCTGTGGTTTCCAGAGTGTCTCCGAGCAACC 300

QY 821 GAGGTGCCCAACAGGGATTTTGGCAACAGCTTCTCAATCTTGAGATACAACTCCACCATC 880

Db 301 GAGGTGCCCAACAGGGATTTTGGCAACAGCTTCTCAATCTTGAGATACAACTCCACCATC 360

QY 881 CAGAAAAGCTTCCACAGGTCTGAATGCTTTCCTCCAGGGTATATCTCCCTCCAGTGTTC 940

Db 361 CAGAAAAGCTTCCACAGGTCTGAATGCTTTCCTCCAGGGTATATCTCCCTCCAGTGTTC 420

QY 941 CACTCGGAGCTGAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCCGATAGC 1000

Db 421 CACTCGGAGCTGAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCCGATAGC 480

QY 1001 AAGTGGCTTTGGCAAGTGAAGTCTGCATCTTGGGCAACCAACCACTGTGGAGGGCAACGCTC 1060

Db 481 AAGTGGCTTTGGCAAGTGAAGTCTGCATCTTGGGCAACCAACCACTGTGGAGGGCAACGCTC 540

QY 1061 ATTGACGCCCAAGTGGGTGCTCACTGCGGCCCACTGCTTCTTCTGTGACCCGGGAGAGGTC 1120

Db 541 ATTGACGCCCAAGTGGGTGCTCACTGCGGCCCACTGCTTCTTCTGTGACCCGGGAGAGGTC 600

QY 1121 CTGGAGGGCTGGAAGGTGTAGCGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCCGATAGC 1180

Db 601 CTGGAGGGCTGGAAGGTGTAGCGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCCGATAGC 660

QY 1181 TCCATTCGAGATCATCATCAACAGCAATTTACACCATGAGGAGGAGCACTATGACATC 1240

Db 661 TCCATTCGAGATCATCATCAACAGCAATTTACACCATGAGGAGGAGCACTATGACATC 720

QY 1241 GCCCTCATGCGGCTGTCCAGGCCCTTGAACCTGTGCGCTGTCACTCCACCTCTGCTTGCCTC 1300

Db 721 GCCCTCATGCGGCTGTCCAGGCCCTTGAACCTGTGCGCTGTCACTCCACCTCTGCTTGCCTC 780

QY 1301 CCCATGATGACAGACCTTTAGCCTCAATGAGACCTGTGCTGGATCAGAGGCTTTGGCA- 1359

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Db      781  TCCTCTGCCCCCAGCCCCCAGACCCCTCTGAGCCCTCGACCTTGTGAGCATCTGTCAAC 840
QY      1360  -----GACCAGGGAGACAGATGACAGACATCCCTCTCTCCGGAGGTGCAG 1408
Db      841  TCATATCCGGGGCCCAAGCTTCTGCAGACAGACATCCCTCTCCGGAGGTGCAG 900
QY      1409  GTCAATCTCATCGACTTCAAGAAATGCAATGACTTGTGCTATGACAGTTACTTTACC 1468
Db      901  GTCAATCTCATCGACTTCAAGAAATGCAATGACTTGTGCTATGACAGTTACTTTACC 960
QY      1469  CCAAGAGTATGATGTGCTGGGAGCTTCTGCTGGGGCAGAGACTCCTGCCAGGGAGACAGC 1528
Db      961  CCAAGAGTATGATGTGCTGGGAGCTTCTGCTGGGGCAGAGACTCCTGCCAGGGAGACAGC 1020
QY      1529  GGGGGGCTCTTGTGTGTGAGCAGAACCAACCGCTGTACTGCGCAGGTGTCAACAGCTGG 1588
Db      1021  GGGGGGCTCTTGTGTGTGAGCAGAACCAACCGCTGTACTGCGCAGGTGTCAACAGCTGG 1080
QY      1589  GGACAGCTGTGCGCCAGAGAAAACAACCTGTGTGTACACCAAAAGTGACAGAAAGTTCTT 1648
Db      1081  GGACAGCTGTGCGCCAGAGAAAACAACCTGTGTGTGTACACCAAAAGTGACAGAAAGTTCTT 1140
QY      1649  CCCTGGATTTACAGCAAGATGGAGCGAGGTGCGATTCAGAAAATCTAAACAGCTGGC 1708
Db      1141  CCCTGGATTTACAGCAAGATGGAG-GCAGGTGGATTCAGAAAATCTAAACAGCTGGC 1199
QY      1709  CTGCTGTCTCTGCACAGCACCGCTGCTGTGA 1739
Db      1200  CTGCTGTCTCTGCACAGCACCGCTGCTGTGA 1230

RESULT 10
US-09-804-156-5
; Sequence 5, Application US/09804156
; Patent No. US20020068320A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P4
; CURRENT APPLICATION NUMBER: US/09/804,156
; PRIORITY FILING DATE: 2001-03-13
; PRIOR FILING DATE: 60/189,025
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-156-5

Query Match      44.8%; Score 782.4; DB 9; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5,5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      892  CCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGCGACT 951
Db      9      CCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCACTGGCGACT 68
QY      952  GAGGGCCATGACCGGGCGGATCGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCCTTG 1011
Db      69  GAGGGCCATGACCGGGCGGATCGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCCTTG 128
QY      1012  GCAAGTGTGCTGTGCACTTCGGACACCAACCATCTGTGAGGACCGCTCATTTGACGCCA 1071
Db      129  GCAAGTGTGCTGTGCACTTCGGACACCAACCATCTGTGAGGACCGCTCATTTGACGCCA 188
QY      1072  GTGGGTGTCTCACTGCGGCCACTGTCTTCTTGTGACCCCGGAGAGAGTCTCTGGAGGGCTG 1131
Db      189  GTGGGTGTCTCACTGCGGCCACTGTCTTCTTGTGACCCCGGAGAGAGTCTCTGGAGGGCTG 248
QY      1132  GAAGGTGTAGCGGGGACCAACGAACTGTGACCAAGTGTGCTGAGGACCGCTCCATTGCCGA 1191
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Db      249  GAAGGTGTATCGCGGGCACCCAGCAACCTGCAACCTGCTTGCCTGAGGACGCTCCATTGCCGA 308
QY      1192  GATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCGCCCTTCATGCG 1251
Db      309  GATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCGCCCTTCATGCG 368
QY      1252  GCTGTCCAAAGCCCTGACCCCTGCGCTCAATCCACCCCTGCTTGCCTCCCATGCGATGG 1311
Db      369  GCTGTCCAAAGCCCTGACCCCTGCGCTCAATCCACCCCTGCTTGCCTCCCATGCGATGG 428
QY      1312  ACAGACCTTTAGCCTCAATGAGACCTGCTGATGACAGGCTTTGGCAAGACCCAGGAGAC 1371
Db      429  ACAGACCTTTAGCCTCAATGAGACCTGCTGATGACAGGCTTTGGCAAGACCCAGGAGAC 488
QY      1372  AGATGACAGACATCCCTCTTCCCGGAGGTGCAAGTCAATCTCATCGACTTCAAGAA 1431
Db      489  AGATGACAGACATCCCTCTTCCCGGAGGTGCAAGTCAATCTCATCGACTTCAAGAA 548
QY      1432  ATGCAATGACTTACTTGTGTATGACAGTTACTTACCCCAAGGATGATGTGCTGGGGA 1491
Db      549  ATGCAATGACTTACTTGTGTATGACAGTTACTTACCCCAAGGATGATGTGCTGGGGA 608
QY      1492  CCTTCGTGGGGCAGACACTTCTGCGCAGGAGACAGCGGGGGCCTCTTGTCTGTGAGCA 1551
Db      609  CCTTCGTGGGGCAGACACTTCTGCGCAGGAGACAGCGGGGGGGCCTCTTGTCTGTGAGCA 668
QY      1552  GAACAACCGCTGTGTACTTGGCAGGTGTCAACAGCTGGGGCAGCAGGCTGTGGCCAGAGAAA 1611
Db      669  GAACAACCGCTGTGTACTTGGCAGGTGTCAACAGCTGGGGCAGCAGGCTGTGGCCAGAGAAA 728
QY      1612  CAAACCTGGTGTGTACACCAAAAGTGACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGGA 1671
Db      729  CAAACCTGGTGTGTACACCAAAAGTGACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGGA 788
QY      1672  GAGC 1675
Db      789  GAAC 792

RESULT 11
US-09-946-633-3
; Sequence 3, Application US/09946633
; Patent No. US20020119925A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/09/946,633
; PRIORITY FILING DATE: 2001-09-06
; PRIOR FILING DATE: 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-633-3

Query Match      44.8%; Score 782.4; DB 10; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5,5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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892 CCACAGGCTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 951
Db 9 CCACAGGCTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 68
952 GAGGGCCATGACCGCGCGGATCTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 1011
Db 69 GAGGGCCATGACCGCGCGGATCTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 128
1012 GCAAGTGAGTCTGCACTTCCGACACCAACCACTCTGTGAGGCGACGCTCATTCAGCCCA 1071
Db 129 GCAAGTGAGTCTGCACTTCCGACACCAACCACTCTGTGAGGCGACGCTCATTCAGCCCA 198
1072 GTGGGTGCTGCACTGCGGCCCACTGCTTCTGTGGAACCGGGAGAAAGTCTCTGAGGGCTG 1131
Db 189 GTGGGTGCTGCACTGCGGCCCACTGCTTCTGTGGAACCGGGAGAAAGTCTCTGAGGGCTG 248
1132 GAGGTGTAGCGGGGACCAAGCAACCTGCACCAAGTTCCTGAGGCGACCTCCATTCGGA 1191
Db 249 GAGGTGTAGCGGGGACCAAGCAACCTGCACCAAGTTCCTGAGGCGACCTCCATTCGGA 308
1192 GATCATCATCAACAGCAATATACCAAGTATGAGGAGGAGCACTATGACATCGCCCTCATGCG 1251
Db 309 GATCATCATCAACAGCAATATACCAAGTATGAGGAGGAGCACTATGACATCGCCCTCATGCG 368
1252 GCTGTCCAAAGCCCTGACCCCTGCTGCTCATCCACCTGCTGCTGCTGCTGCTGCTGCTG 1311
Db 369 GCTGTCCAAAGCCCTGACCCCTGCTGCTCATCCACCTGCTGCTGCTGCTGCTGCTGCTG 428
1312 ACAGACCTTTAGCTTCAATGAGACCTGCTGCTGATCACAGGCTTTGGCAAGACCAAGGAGAC 1371
Db 429 ACAGACCTTTAGCTTCAATGAGACCTGCTGCTGATCACAGGCTTTGGCAAGACCAAGGAGAC 488
1372 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATCGACTTCAAGAA 1431
Db 489 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATCGACTTCAAGAA 548
1432 ATGCAATGACTACTTGGTCTATGACAGTACCTTACCCCAAGATGATGCTGCTGGGA 1491
Db 549 ATGCAATGACTACTTGGTCTATGACAGTACCTTACCCCAAGATGATGCTGCTGGGA 608
1492 CCTTCTGCGGGGAGAGACTCTGCGGAGGAGACAGCGGGGGCTCTTCTGCTGTGAGCA 1551
Db 609 CCTTCTGCGGGGAGAGACTCTGCGGAGGAGACAGCGGGGGCTCTTCTGCTGTGAGCA 668
1552 GAAACACCGCTGTACTCTGCGAGGTGTACAGGCTGGGCAAGGCTGTGCTGGCCAGAGAA 1611
Db 669 GAAACACCGCTGTACTCTGCGAGGTGTACAGGCTGGGCAAGGCTGTGCTGGCCAGAGAA 728
1612 CAACCTGGTGTATACCAAGGTGACAGAGTCTTCCCTGGATTTACAGCAAGATGGA 1671
Db 729 CAACCTGGTGTATACCAAGGTGACAGAGTCTTCCCTGGATTTACAGCAAGATGGA 788
1672 GAGC 1675
Db 789 GAAC 792

RESULT 12
US-10-319-519-5
; Sequence 5, Application US/10319519
; Publication No. US20030175938A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; FILE REFERENCE: PT005P5
; CURRENT APPLICATION NUMBER: US/10/319,519
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 09/597,842
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/597,843

PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 10/067,761
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 09/946,633
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 09/804,156
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US00/12207
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/189,025
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/162,979
; PRIOR FILING DATE: 1999-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-319-519-5
Query Match 44.8%; Score 782.4; DB 13; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5.5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
892 CCACAGGCTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 951
Db 9 CCACAGGCTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 68
952 GAGGGCCATGACCGCGCGGATCTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 1011
Db 69 GAGGGCCATGACCGCGCGGATCTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 128
1012 GCAAGTGAGTCTGCACTTCCGACACCAACCACTCTGTGAGGCGACGCTCATTCAGCCCA 1071
Db 129 GCAAGTGAGTCTGCACTTCCGACACCAACCACTCTGTGAGGCGACGCTCATTCAGCCCA 188
1072 GTGGGTGCTGCACTGCGGCCCACTGCTTCTGTGGAACCGGGAGAAAGTCTCTGAGGGCTG 1131
Db 189 GTGGGTGCTGCACTGCGGCCCACTGCTTCTGTGGAACCGGGAGAAAGTCTCTGAGGGCTG 248
1132 GAAAGTGTATGCGGGGACCAAGCAACCTGCAACAGTTCCTGAGGCGACCTCCATTCGCGA 1191
Db 249 GAAAGTGTATGCGGGGACCAAGCAACCTGCAACAGTTCCTGAGGCGACCTCCATTCGCGA 308
1192 GATCATCATCAACAGCAATATACCAAGTATGAGGAGGAGCACTATGACATCGCCCTCATGCG 1251
Db 309 GATCATCATCAACAGCAATATACCAAGTATGAGGAGGAGCACTATGACATCGCCCTCATGCG 368
1252 GCTGTCCAAAGCCCTGACCCCTGCTGCTCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
Db 369 GCTGTCCAAAGCCCTGACCCCTGCTGCTCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 428
1312 ACAGACCTTTAGCTTCAATGAGACCTGCTGCTGATCACAGGCTTTGGCAAGACCAAGGAGAC 1371
Db 429 ACAGACCTTTAGCTTCAATGAGACCTGCTGCTGATCACAGGCTTTGGCAAGACCAAGGAGAC 488
1372 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATCGACTTCAAGAA 1431
Db 489 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATCGACTTCAAGAA 548
1432 ATGCAATGACTACTTGGTCTATGACAGTACCTTACCCCAAGATGATGCTGCTGGGA 1491
Db 549 ATGCAATGACTACTTGGTCTATGACAGTACCTTACCCCAAGATGATGCTGCTGGGA 608
1492 CCTTCTGCGGGGAGAGACTCTGCGGAGGAGACAGCGGGGGCTCTTCTGCTGTGAGCA 1551
Db 609 CCTTCTGCGGGGAGAGACTCTGCGGAGGAGACAGCGGGGGCTCTTCTGCTGTGAGCA 668
1552 GAAACACCGCTGTACTCTGCGAGGTGTACAGGCTGGGCAAGGCTGTGCTGGCCAGAGAA 1611
Db 669 GAAACACCGCTGTACTCTGCGAGGTGTACAGGCTGGGCAAGGCTGTGCTGGCCAGAGAA 728
1612 CAACCTGGTGTATACCAAGGTGACAGAGTCTTCCCTGGATTTACAGCAAGATGGA 1671
Db 729 CAACCTGGTGTATACCAAGGTGACAGAGTCTTCCCTGGATTTACAGCAAGATGGA 788
1672 GAGC 1675
Db 789 GAAC 792

Db 669 GAACACCGCTGCTACCTGGAGGTGTACCCAGCTGGGGCAAGGCTGTGGCCAGAGAAA 728
Qy 1612 CAAACCTGGTGTGTACACCAAGTGTACAGAGTCTTCCCTGGATTTACAGCAAGATGGA 1671
Db 729 CAAACCTGGTGTGTACACCAAGTGTACAGAGTCTTCCCTGGATTTACAGCAAGATGGA 788
Qy 1672 GAGC 1675
Db 789 GAAC 792

RESULT 13
US-10-125-459-3
; Sequence 3, Application US/10125459
; Publication No. US20020192800A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-459-3

Query Match 44.8%; Score 782.4; DB 14; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5.5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 892 CCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 951
Db 9 CCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 68

Qy 952 GAGGCCCATGACCGGGCGGATCGTGGGAGGGCGCTGGCCCTCGGATAGCAAGTGGCCCTTG 1011
Db 69 GAGGCCCATGACCGGGCGGATCGTGGGAGGGCGCTGGCCCTCGGATAGCAAGTGGCCCTTG 128

Qy 1012 GCAAGTGTGCTGCACTTCGGCACCACCAATCTGTGGAGGCGCTCATGAGCCCA 1071
Db 129 GCAAGTGTGCTGCACTTCGGCACCACCAATCTGTGGAGGCGCTCATGAGCCCA 188

Qy 1072 GTGGGTGTCTACTGCGGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 1131
Db 189 GTGGGTGTCTACTGCGGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 248

Qy 1132 GAAGGTGTACCGGGGCAACAGCACTGTGACCGGAGAGGTCTCTGGAGGGCTG 1011
Db 249 GAAGGTGTACCGGGGCAACAGCACTGTGACCGGAGAGGTCTCTGGAGGGCTG 248

Qy 1192 GATCATCATCACAGCAATTAACCGATGAGGAGGAGCACTATGACATGCGCCCTCATGG 1251
Db 309 GATCATCATCACAGCAATTAACCGATGAGGAGGAGCACTATGACATGCGCCCTCATGG 368

Qy 1252 GCTGTCCAAAGCCCTGACCCCTGTCCGCTCACATCCACCCCTGTGCTCCCTCCCATGCG 1311
Db 369 GCTGTCCAAAGCCCTGACCCCTGTCCGCTCACATCCACCCCTGTGCTCCCTCCCATGCG 428

Qy 1312 ACAGACCTTTAGCTCTCAATGAGACCTGTGTGATCAAGGCTTTGGCAAGACCAAGGAGAC 1371
Db 429 ACAGACCTTTAGCTCTCAATGAGACCTGTGTGATCAAGGCTTTGGCAAGACCAAGGAGAC 488

Qy 1372 AGATGACAGACATCCCTTCTCCCGGAGGTGACAGTCAATCTCATCTCACTTCAAGAA 1431
Db 489 AGATGACAGACATCCCTTCTCCCGGAGGTGACAGTCAATCTCATCTCACTTCAAGAA 548

Qy 1432 ATGCAATGACTACTTGTCTATGACAGTGTACCTTACCCCAAGGATGATGTGTCTGGGA 1491
Db 549 ATGCAATGACTACTTGTCTATGACAGTGTACCTTACCCCAAGGATGATGTGTCTGGGA 608

Qy 1492 CTTTGTGGGGGAGAGACTCTCTGCGGAGGAGACAGCGGGGGGCTTCTGTGTGAGCA 1551
Db 609 CTTTGTGGGGGAGAGACTCTCTGCGGAGGAGACAGCGGGGGGCTTCTGTGTGAGCA 668

Qy 1552 GAACAAACCGCTGTCTGTCAGGTTGTCACAGTGTGTCAGGCTGTGCGCCAGAGAAA 1611
Db 669 GAACAAACCGCTGTGTCAGGTTGTCACAGTGTGTCAGGCTGTGCGCCAGAGAAA 728

Qy 1612 CAAACCTGTGTGTACACCAAGTGTGACAGAGTTCCTTCCCTGGATTTACAGCAAGATGGA 1671
Db 729 CAAACCTGTGTGTACACCAAGTGTGACAGAGTTCCTTCCCTGGATTTACAGCAAGATGGA 788

Qy 1672 GAGC 1675
Db 789 GAAC 792

RESULT 14
US-10-067-761-5
; Sequence 5, Application US/10067761
; Publication No. US2002019701A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P4
; CURRENT APPLICATION NUMBER: US/10/067,761
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 09/804,156
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,025
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-761-5

Query Match 44.8%; Score 782.4; DB 14; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5.5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 892 CCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 951
Db 9 CCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 68

Qy 952 GAGGCCCATGACCGGGCGGATCGTGGGAGGGCGCTGGCCCTCGGATAGCAAGTGGCCCTTG 1011
Db 69 GAGGCCCATGACCGGGCGGATCGTGGGAGGGCGCTGGCCCTCGGATAGCAAGTGGCCCTTG 128

Qy 1012 GCAAGTGTGCTGCACTTCGGCACCACCAATCTGTGGAGGCGCTCATGAGCCCA 1071
Db 129 GCAAGTGTGCTGCACTTCGGCACCACCAATCTGTGGAGGCGCTCATGAGCCCA 188

Qy 1072 GTGGGTGTCTACTGCGGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 1131
Db 189 GTGGGTGTCTACTGCGGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCACTGGGACT 248

Qy 1132 GAAGGTGTACCGGGGCAACAGCACTGTGACCGGAGAGGTCTCTGGAGGGCTG 1011

301 CAAACAGCAATTACACCGATGAGGAGGACGACTATGACATCGCCCTCATGCGGCTGTTCAA 360

1261 GCCCTGACCC 1271

361 GCCCCTTGACC 371

RESULT 2

US-09-008-271A-18

Sequence 18, Application US/09008271A

Patent No. 6203979

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Hillman, Jennifer L.

Yue, Henry

Guegler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271A

FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mohan-Peterson, Sheela

REGISTRATION NUMBER: 41,201

REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 2038 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: COLNNOT13

CLONE: 1337018

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-008-271A-18

Query Match 11.1%; Score 193.2; DB 3; Length 2038;

Best Local Similarity 55.8%; Pred. No. 8.3e-39;

Matches 435; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

924 TCTCCCTCCAGTTTCCCACTGCGAGCTGAGGCGCATGACCGGCGGATCGTGGAGGCG 983

759 TCTCCCTGCACTGTCTTGCCTGTGGGAGAGCTGAGACCCCTGTTGGTGGTGGG 818

984 CGCTGGCTCGATAGCAAGTGGCTTGCAGTCACTGCTGCGCACCCACCA 1043

819 AGGAGGCTCTGTGAATTCTTGGCTTGGCAGGTGAGTATCGACGACCAACGACG 878

1044 TCTGTGGAGGACCGCTCATTTGACGCGCAGTGGGTCTCACTGCGGCCCACTCTCTTCG 1103

879 TCTGTGGAGGAGCATCTTGGACCCCACTGGGCTCTCAAGCAGCCCACTGCTTC 934

1104 TGACCCGCGGAGAGGTCCTGGAAGGCTGGAAGGTGTACGCGGCGCACAGCAACTGCACC 1163

935 --AGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGCGAGGCTCAGACAACTGGCA 992

1164 AGTTGCTGAGGAGCGCTCCATTGCGGAGATCATCATCAACAGCAATTACACGATGAGG 1223

993 GCTTCCC--ATCCCTGGCTGTGGCCAAAGATCATCATTTGAATTCAACCCCATGACC 1049

1224 AGGACGACTATGACATCGCCCTCATGCGGCTGTCCAAGCCCTGACACCTGTGCCCTCACA 1283

1050 CCAAGACATGACATCGCCCTCATGAGGTGCAAGTTCCTCCACTCCTCTCTCAGGCACAG 1109

1284 TCACCCCTGCTTGCCTCCCATGATGGAAGACAGACCTTTAGCCTCAATGAGACCTGCTGGA 1343

1110 TCAGGCCCATCTGCTGCTGCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGA 1169

1344 TCACAGCTTTGGCAGAGCAGGAGGACAGATGACAGACATCCCTCTCTCCGCGAGG 1403

1170 TCATTGGATGGGCTTTTACGAAGCAGAAATGGAGGGAAGATGTCGACATATCTGTCGAGG 1229

1404 TGCAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTTCTGCTATGACAGTTTACC 1463

1230 CGTCAGTCCAGGTCAATTGACAGACACGCTGCAATGACAGAGTGCCTACAGGGGAG 1289

1464 TTACCCCAAGGATGATGCTGCTGGGACCTTCTGTTGGGCGAGAGACTTCTTCCAGGGAG 1523

1290 TCACCGAGAAAGATGATGTCAGGCTCCCGGAAGGGGTGTGGAACACCTGCCAGGGTG 1349

1524 ACAGCGGGGCTCTTGTCTGTGAGCAGAAACACCGCTGTACTTGCAGGTGTACCA 1583

1350 ACAGTGGTGGGCTCTGATGT---ACCAATCTGACCCAGGATATACCAAGGTCTCAGCCT 1406

1584 GCTGGGCGACAGGCTGTGGCCAGAGAAACAACTGCTGTGTATACCAAAAGTACAGAA 1643

1407 GCTGGGCTATGCTGTGGGGCCCGGAGCAGGATATACCAAGGTCTCAGCCT 1466

1644 TTCTTCCCTGGATTTACAGCAAGATGAGAGCGAGGTGCGGATTCAGAAAATCTTAAACAG 1703

1467 ATCTCAACTGGATCTCAAAATGTCGGAAGGCTGAGCTGTAATGCTGCTGCCCTTTGCAG 1526

RESULT 3

US-09-656-002-1

Sequence 1, Application US/09656002

Patent No. 6455668

GENERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Gish, Kurt

APPLICANT: Wilson, Keith

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

FILE REFERENCE: A-69108/DJB/JJD/AMS

CURRENT APPLICATION NUMBER: US/09/656,002

CURRENT FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: US 09/525,993

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 09/493,444

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: PCT/US 00/07044

PRIOR FILING DATE: 2000-03-15

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patent in version 3.0

SEQ ID NO 1

LENGTH: 2079

TYPE: DNA

ORGANISM: Homo sapiens

US-09-656-002-1

Query Match 11.1%; Score 193.2; DB 4; Length 2079;

Best Local Similarity 55.8%; Pred. No. 8.3e-39;

Matches 435; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

924	Qy	TTCTCCCTCCAGTGTTCCTCCACTGCGGACTGAGGGCCATGACACGGGGCGGATCTGTGGGAGGGG	983
925	Qy	TTCTCCCTCCAGTGTTCCTCCACTGCGGACTGAGGGCCATGACACGGGGCGGATCTGTGGGAGGGG	984
774	Db	TTCTCCCTGCACCTGTCTTGGCTGTGGGAAGAGCCCTGAGAGCCCCCGCTGTGTGGTGGGTGGGG	833
984	Qy	CGCTGGCCCTCGGATAGCAAGTGGCCCTTTGGCAAGTGAAGTCTGCACTTTCGGGCACACCCACCA	1043
834	Db	AGAGGGCTCTGTGGATTTCTTGGCTTTGGCAAGTGAAGTCTGCACTTTCGGGCACACCCACCA	893
1044	Qy	TTCTGTGGAGCAAGCTCATTGAGCCCGCACTGGGTGCTCACTGCGGCCACTGTTCTTCTTCG	1103
894	Db	TTCTGTGGAGGAGCATCCTCGACCCCACTGGGTCTCTCACGGCAGGCCACTGCTTCTC---	949
1104	Qy	TGACCCGGGAGAGGTCCTCGAGGGCTGGAGGTGTACGGGGGCAACAGGAACTGTGCACC	1163
950	Db	--AGGAACAATACCGATGTGTTCAACTGGGAAGGTGGGGCAGGCTCAGACAAACTGGGCA	1007
1164	Qy	AGTTGCTTGAGGGCAGCCTCCATTGCGGAGATCATCATCAACAGCAATTCACACCGATGAGG	1223
1008	Db	GCCTTCCC---ATCCCTGGCTGTGGCCCAAGATCATCATCTTGAATTCACCCCATGTACC	1064
1224	Qy	AGGACGACTATGACATCGCCCTCATGCGGCTGTCCAGGCCCTGACCCCTGTCGGCTCACA	1283
1065	Db	CCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTTCCCACCTCACTTTCTCAGGCACAG	1124
1284	Qy	TCCACCTCTGTGCTCTCCCATGATGGAACAGACTTCTTAGCTCAATGAGACCTGTCTGGA	1343
1125	Db	TCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGGCCACCCCACTCTGGA	1184
1344	Qy	TCACAGGCTTTGGCAAGACCAAGGAGACAGATGACAGACATCCCCCTTCTCCTCCGGGAGG	1403
1185	Db	TCATTTGATGGGGCTTTACGAAGCAGAAATGGAGGGAAGATGTTGACATACTGCTGCAGG	1244
1404	Qy	TGCAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGTCTATGACAGTTTACC	1463
1245	Db	CGTCAGTCTCAGGTCAATTTGACAGCACACGGTGCATATGACAGATGCGTACAGGGGGAG	1304
1464	Qy	TTACCCCAAGATGATGTGTCTGGGACCTTCTGTGGGGCAGAGACTCTCTCCAGGGAG	1523
1305	Db	TCACCGAAGAATGATGTGTGAGGCATCCCGGAAGGGGGTGTGGAACACTCTGCCAGGGTG	1364
1524	Qy	ACAGGGGGGGCCTTGTCTGTGTAGCAGAAACACCCGCTGGTACTCTGGCAGGTGTCACCA	1583
1365	Db	ACAGTGTGTGGGCCCTGATGT---ACCAATCTGACAGTGGCATGTGTGTGGGCATCGTTA	1421
1584	Qy	GCTGGGCAACAGGCTGTGGCCAGAGAAACAACTGGTGTGTACACCAAAAGTGACACAAG	1643
1422	Db	GCTGGGGCTATGGCTGTGGGGGCCCGAGCACCCACAGAGTATACACCAAGTCTCAGCCT	1481
1644	Qy	TTCTTCCCTGGATTTACAGCAAGATGGAGCGAGGTGCGATTTCAGAAAAATCTCTAACCAAG	1703
1482	Db	ATCTCAACTGGATCTCAAACTCTGGGAAGGCTGAGCTGTAAATGTCTGTGCCCTTTTCAG	1541

```

RESULT 4
US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TAGD-12 gene
US-09-518-046-1

Query Match      10.4%; Score 181.2; DB 3; Length 2413;
Best Local Similarity 55.6%; Pred. No. 8.7e-36;
Matches 414; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

Qy 953 AGGCGCANGACCGGGCGGATCGTGGGAGGGCGCTGGCTCGGATAGCAAGTGGCCTTGG 1012
Db |||||
Qy 777 AGGGGCTACAGCTCAAGCATGTGGGGTGGAAACATGTCTTGTCTCTCGCAGTGGCCCTGG 836
Db |||||
Qy 1013 CAAGTGAATCTGCATCTGGCACCACCAATCTGTGGAGGCGACGCTCATTTGACGCCAG 1072
Db |||||
Qy 837 CAGGCCAGCCCTCAGTTTCCAGGGCTACCACCTGTGGGGGGCTCTGTTCATCAGCCCCCTG 896
Db |||||
Qy 1073 TGGGTGCTCACTGCGGCCCACTGCTTCTCGTGACCCGGGAGAGGTCTCTGGAGGGCTGG 1132
Db |||||
Qy 897 TGGATCATCACTGCTGCACACTGTGTTATG-----ACTTGTACCTCCCAAGTCATGG 950
Db |||||
Qy 1133 AAGGTGTACCGGGCACACAGCAACCTGSCACAGTGTGCTGAGGCGAGCCTCCATTCGCCGAG 1192
Db |||||
Qy 951 ACCATCCAGGTGGGTCTAGTTTCCCTGTGTGCAATCCAGCCCATCCCACTTGGTGGAG 1010
Db |||||
Qy 1193 ATCA---TCATCAACAGCAATTTACACCGATGAGGAGCAACATATGATGATGCGCCTCATG 1249
Db |||||
Qy 1011 AAGATTGTCTACCAAGCAAGTACAGCCAAAGAGGCTGGGGCAATGACATGCGCCCTTATG 1070
Db |||||
Qy 1250 CGGCTGTCCAAAGCCCTGACCTGTGCGCTCAATCCACCTGCTGTCCCTCCCATGCAT 1309
Db |||||
Qy 1071 AAGCTGGCCGGGCCACTCAGCTTCATGAATGATTCAGGCTGTGTGCTTGGCCCTCCCACTCT 1130
Db |||||
Qy 1310 GGACAGACCTTTTAGCCTCAATGAGACCTGCTGGATCAACAGGCTTTGGCAAGACACGGAG 1369
Db |||||
Qy 1131 GAAGAGAACTTCCCGATGGAAGTGTCTTGGAGTTCAGATGGGGGGCCACAGAGAT 1190
Db |||||
Qy 1370 ACAGATGACAAAGACATCCCTCTTCTCCGGGAGGTGCGAGTCAATCTCATGCTTCAAG 1429
Db |||||
Qy 1191 GGAGGTGAC---GGCTCCCTGTCTCTGAAACCAACGCGGCCGCTCCCTTTGATTTCCAAACAAG 1247
Db |||||
Qy 1430 AAATGCAATGACTACTTGGTCTATGACAGTTTACCTTACCCCAAGGATGATGTGTCTGGG 1489
Db |||||
Qy 1248 ATCTGCAACCAACAGGACGTGTACGGTGGCATCATCTCCCTCCATGCTCTTGGCGCGGC 1307
Db |||||
Qy 1490 GACTCTCTGGGGCGACAGACTCTCTGCGCAGGGAGACAGCGGGGGGCTCTTGTCTGTGAG 1549
Db |||||
Qy 1308 TACTGTACGGGTGGCGTGAACAGCTGCCAGGGGAGACAGGGGCGGCCCTGTGTGTCA 1367
Db |||||
Qy 1550 CAGAACAAACGCTGGTCTCTGGCAGGTGTCAACAGTCTGGGGCAACAGGCTGTGGCCACAGAG 1609
Db |||||
Qy 1368 GAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACACAGCTTTGGCATCGGCTGGCGCAGAGTG 1427
Db |||||
Qy 1610 AACAAACCTGGTGTATACCAACAAAGTACAGAGATTTCTTCCCTGGATTTACAGCAAGATG 1668
Db |||||
Qy 1428 AACAGGCTGGGGGTGACACCGGTGTCACTCTCTCTTGGATCGATCCACAGCAGATG 1487
Db |||||
Qy 1670 GAGAGCGAGGTGGCATTCAGAAAA 1693
Db |||||
Qy 1488 GAGAGAGACCTAAAACCTGAAGA 1511
Db |||||

RESULT 5
US-08-807-151-2
; Sequence 2, Application US/08807151
; Patent No. 6043033
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,151
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0227 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1077 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SCORN0T01
CLONE: 556016
US-08-807-151-2

Query Match 10.1%; Score 177.4; DB 3; Length 1077;
Best Local Similarity 54.5%; Pred. No. 5.6e-35;
Matches 399; Conservative 0; Mismatches 327; Indels 6; Gaps 2;

QY 969 GGATCGTGGGAGGCGCTCGGATAGCAAGTGGCTTGGCAAGTGAGTCTGCACT 1028
DB 237 GGATCGTGGGCGGAGAGCGCGCTCCCGGGGCTGGCCCTGGCAGTGCAGCTGACG 296
QY 1029 TCGGCACACCCACATCTGTGGAGCAGCTCATTCAGCCAGTGGGTGCTCACTGCCG 1088
DB 297 TCCAGAGCTCCACGTGTGCGAGGCTCCATCATCACCCCGAGTGGATCGTGAAGCG 356
QY 1089 CCGACTGCTTCTGTGACCGGAGAGGCTCTGGAGGCTGGAGGTGTAACGGGCA 1148
DB 357 CCGACTGCTGGAACCTCTTAACAATCCATGGCATTTGACGCGCATTTGGGGGATT 416
QY 1149 CCAGCAACCTGCACAGTGTGCTGAGGAGGCTCCATTCGCGAGA---TCATCATCA 1205
DB 417 TGAGACATCTTTCATGTTCTATGAGCGGATACCAAGTAGAAAAAGTGAATTCATC 476
QY 1206 GCAATTCACGATGAGAGGAGCAGTATGATCGCCCTCATGCGGCTGCAAGCCCC 1265
DB 477 CAAATATGACTCCAGACCAAGAACATGCAATTCGCTGATGAAGCTGCAAGAGCTC 536
QY 1266 TGACCTGTCGCTCACATCCACCTGCTGCTCCCATGATGATGAGAGACCTTTAGCC 1325
DB 537 TGACTTTCAAGCACTAGTGAACAGTGTGTCTGCCAACCCAGGCAATGCTGACG 596
QY 1326 TCAATGAGACCTGTGGATCAAGGCTTTGGCAAGACCCAGGAGAGCAGATGAAGACAT 1385
DB 597 CAGACAGCTCTGCTGGATTTCCGGGTGGGGGCCACCGAGGAGA--AAGGAGAGACT 653
QY 1386 CCCCCCTTCTCGGGAGGTGCGAGTCAATCTCATGCTTCAAGAAATGCAATGACTACT 1445
DB 654 CAGAAAGTGTGAACCTGCGAAGTGTCTTCTCATTTGAGACACAGAGATGCAACAGCAT 713
QY 1446 TGCTCTATGACATTTACCTTACCCCAAGATGATGTGCTGGGACCTTCTGTGGGGCA 1505

10.1%; Score 177.4; DB 4; Length 1077;
Best Local Similarity 54.5%; Pred. No. 5.6e-35;
Matches 399; Conservative 0; Mismatches 327; Indels 6; Gaps 2;

QY 969 GGATCGTGGGAGGCGCTCGGATAGCAAGTGGCTTGGCAAGTGAGTCTGCACT 1028
DB 237 GGATCGTGGGCGGAGAGCGCGCTCCCGGGGCTGGCCCTGGCAGTGCAGCTGACG 296

714 ATGCTATGACAACCTGATACACACAGCCATGATCTGTGCGGGCTTCTCGAGGGGAACG 773
1506 GAGACTCCTGCCAGGAGAGCAGCGGGGGGCTCTTGTGCTGTGAGCAGACACACCGCTGGT 1565
774 TCGATTTCTTCCAGGGTGACAGTGGAGGGCTTCTGCTCACTTGAAGACAAATATCTGGT 833
1566 ACCTGGCAGGTGTCAACAGCTGGGGGCAAGGCTGTGGCCAGAGAAACAAACCTGGTGTGT 1625
834 GGCTGATAGGGGATACAAAGCTGGGGTCTGGCTGTGCAAAAGCTTACAGACCAAGGTGT 893
1626 ACACCAAGTGCACAGAGTCTTCCCTGGATTTTACACAGATGAGAGCGAGGTGCGAT 1685
894 ACGGAAATGTGATGGTATTACCGACTGGATTTATCGACAAATGAGGGCAGACCGCTAAT 953
1686 TCAGAAAATCCT 1697
954 CCACATGGTCTT 965

RESULT 6
US-09-478-957-2
; Sequence 2, Application US/09478957
; Patent No. 6350448
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/478,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/807,151
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0227 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1077 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SCORN0T01
; CLONE: 556016
US-09-478-957-2

Query Match 10.1%; Score 177.4; DB 4; Length 1077;
Best Local Similarity 54.5%; Pred. No. 5.6e-35;
Matches 399; Conservative 0; Mismatches 327; Indels 6; Gaps 2;

QY 969 GGATCGTGGGAGGCGCTCGGATAGCAAGTGGCTTGGCAAGTGAGTCTGCACT 1028
DB 237 GGATCGTGGGCGGAGAGCGCGCTCCCGGGGCTGGCCCTGGCAGTGCAGCTGACG 296

QY 1029 TCGGACACCCACATCTGTGGAGGACCGCTCAATTGACGCCCGGAGTGGTGTCTCACTGCCG 1088
Db |||||
297 TCAGAACGTCACGCTGTGGAGGCTCCATCATACACCCCGAGTGGATCGTGACAGCG 356
QY 1089 CCACACTGCTTCTTCTGTGACCCGGAGAGGCTCTCGAGGGCTGGAAGTGTACGCGGCA 1148
Db |||||
357 CCACACTGCTGGAACACCTCTTAACATCCATCGGCAATGACCGGCAATTTGCGGGGATTT 416
QY 1149 CCAGCAACCTGCACGATTTGCTGAGGACGCTCCATTTGCCGAGA---TCATCATCAACA 1205
Db |||||
417 TGAGACAAATCTTTTCATGTTCTATGAGCGCGATACCAAGTAGAAGAAAGTATTTCTCATC 476
QY 1206 GCAATTACCGATGAGGAGGACGATATGATCGCCCTCATCGGCTGTCCAGCCCC 1265
Db |||||
477 CAAATATTGACTCCAGACCAAGAACATGACATGCGCTGTGATGAAGCTGCAGAGCCTC 536
QY 1266 TGACCCCTGTCGCTCAACCTCCCTCTTGTGCTCCCATGTCATGAGACACCTTTAGCC 1325
Db |||||
537 TGACTTTCAAGACCTAGTGAACAGTGTGTCTGCCAACCCAGGATGATGCTGCAGC 596
QY 1326 TCAATGAGACCTGCTGATCAAGGCTTTGGCAAGACCGAGGACACAGATGACAGACAT 1385
Db |||||
597 CAGAACAGCTCTGCTGATTTCCGGGTGGGGGCCACCGAGGAGA---AAGGGAAGACCT 653
QY 1386 CCCCCTTCTCCGGAGGTGACGTCATCTCATGACTTCAAGAAATGCAATGACTACT 1445
Db |||||
654 CAGAAGTGTGAAAGCTGCAAGGTGCTTCTCATTTGAGACACAGAGATGCAACGACGAT 713
QY 1446 TGCTCTATGACAGTTACTTACCCCAAGAGTGTGTGTGCTGGGGACCTTCTGGGGGCA 1505
Db |||||
714 ATGCTATGACACCTGATACACACGACCATGATCTGTGCGGCTTCTGAGGGGACG 773
QY 1506 GAGACTCTCCGAGGAGACAGCGGGGGCTCTTGTGTGAGAGAGAACCAACGCTGTGT 1565
Db |||||
774 TCGATTCTCCAGGGGTGACAGTGGAGGGGCTTCTGTGCTTCTGCAAGAAACATATCTGT 833
QY 1566 ACTGGCAGTGTACACGCTGGGACAGCTGTGCGCAGAGAACAAACCTGTGTGT 1625
Db |||||
834 GGCTGATAGGGATACAAAGCTGGGGTTCTGGCTGTGCAAGCTTACAGACCCAGAGTGT 893
QY 1626 ACACCAAGTGACAGAGTCTTCCCTGGATTTACAGCAAGATGAGAGCGAGTGGAT 1685
Db |||||
894 ACGGATGTGATGGTATTACGGACTGGATTTATCGAATGAGGGGACAGCGCTAAT 953
QY 1686 TCAGAAATCCT 1697
Db |||||
954 CCACATGGTCTT 965

RESULT 7

US-09-342-749-1
; Sequence 1, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCES: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

Query Match 10.1%; Score 176.4; DB 3; Length 1479;
Best Local Similarity 54.9%; Pred. No. 1.1e-34;
Matches 392; Conservative 0; Mismatches 316; Indels 6; Gaps 2;

QY 969 GATCGTGGAGGGGCGCTGCGCTCGGATGAGAGTGGCTTGGCAGAGTGTGCACT 1028
Db |||||
764 GATCGTGGGCGCGAGAGCGCGCTCCCGGGGCGCTGCGAGTGTGCACTGCACTG 823
QY 1029 TCGGCACCAACCCACATCTGTGGAGGACCGCTCATTTGACGCCCGGAGTGGTGTCTCACTGCCG 1088
Db |||||
824 TCAGAACGTTCCACGTTGTGGAGGGCTTCATCATCATCCCCCAGTGGATCGTGACAGCCG 883
QY 1089 CCACACTGCTTCTTCTGTGACCCCGGAGAGGTCCTCGAGGGCTGGAAGTGTAGCGGGCA 1148
Db |||||
884 CCACACTGGTGGAAAAACCTCTTAAACATTCATTCATTCGACGCAATTTCCGGGATTT 943
QY 1149 CGAGCAACCTGCACGATTTGCTGAGGAGCTTCCATTTGCCGAGA---TCATCATCAACA 1205
Db |||||
944 TGAGACAAATCTTTTCATGTTCTATGAGCGCGATACCAAGTAGAAGAAAGTATTTCTCATC 1003
QY 1206 GCAATTACCGATGAGGAGGACGATGACATCGCCCTCATGCGGCTGTCCAGCCCC 1265
Db |||||

US-09-342-749-1

1004 CAAATATGACTCCAAAGCAAGAAACAATGACATTTGGCTGATGAAGCTGCAAGAGCCTC 1063
1266 TGACCTTGTCCGCTCAGATCCACCTGCTTGGCTCCCAATGATGACAGACCTTTAGCC 1325
1064 TGACTTTCAACGACCTAGTGAACCAAGTGTCTGCTCCCAACCCAGGATGATGCTGAGC 1123
1326 TCAATGAGACCTGCTGATCAGAGCTTTGGCAAGACCAAGGAGAGAGATGACAAGACAT 1385
1124 CAGAACAGCTCTGCTGATTTCCGGTGGGGGCCACCGAGAGA---AAGGAGAGACCT 1180
1386 CCCCCTTCCTCCGGAGGTGAGTCAATCTCATGACTTCAAGAAATGCAATGACTACT 1445
1181 CAGAAGTGTGAAAGCTGCAAGTGTCTTCTCATTTGAGACACAGAGATGCAACAGCAGAT 1240
1446 TGGTCTATGACAGTTACTTACCCCAAGGATGATGTGCTGGGACCTTCTGGGGGCA 1505
1241 ATGTCTATGACAACTGATACACAGCATGATCTGTGCGGCTTCTGAGGGGAGCG 1300
1506 GAGACTCTCTCCAGGAGAGACAGCGGGGGCTTCTGTGTGAGCAGAAACAACTGCTGT 1565
1301 TCGATTCTTCCAGGGTGACAGTGGAGGCTCTGTGCTCACTTCGAAGAAACAATATCTGGT 1360
1566 ACCTGGAGGTGTACAGCTGGGCGACAGCTGTGGCAGAGAAACAACTGCTGT 1625
1361 GGCTGATAGGGGATACAGCTGGGGTCTGCTGTGCAAGCTTACAGACAGGAGTGT 1420
1626 ACACCAAGTACAGAGTCTTCTCCCTGATTTACAGCAAGATGAGAGCGAGG 1679
1421 ACGGAATGTGTGATGATTACAGACTGGATTTATCGAATATGAGGCGAGCG 1474

RESULT 8

US-09-691-840-1
; Sequence 1, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: THPRS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1466)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1471)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329.
; NAME/KEY: allele

LOCATION: (478)
; OTHER INFORMATION: This base can be G or A with G being the more
; OTHER INFORMATION: common allele. The codon will change from Val to
; OTHER INFORMATION: Met.
; NAME/KEY: allele
; LOCATION: (777)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. The codon is unaffected with both
; OTHER INFORMATION: alleles encoding Gly.
; NAME/KEY: allele
; LOCATION: (768)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (834)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (625)
; OTHER INFORMATION: This base can be T or A with T being the more
; OTHER INFORMATION: common allele. The codon will change from Phe to Ile
; US-09-691-840-1

Query Match 10.18; Score 176.4; DB 4; Length 1479;
Best Local Similarity 54.9%; Pred. No. 1.1e-34;
Matches 392; Conservative 0; Mismatches 316; Indels 6; Gaps 2;
QY 969 GGATCGTGGAGGGCGCTGCGCTCGGATAGCAGTGGCTTGGCAAGTGAAGTGTGCACT 1028
DB 764 GGATCGTGGAGGGCGGAGAGCGCGCTCCCGGGGGCTGCGCTGAGCTCAGCTGCAAG 823
QY 1029 TCGGCACACCCACATCTGTGGAGGAGGCTGATGAGAGCCAGTGGTGTCTGCTGCG 1088
DB 824 TCCAGAAAGCTCCAGTGTGGAGGAGGCTCCATCATCACCCCGAGTGGATCGTGAAGCG 883
QY 1089 CCCACTGCTTCTTCTGTCGACCGGGAGAGAGTCTCTGGAGGCTGGAAGTGTACCGGGCA 1148
DB 884 CCCACTGCTGGAGAAACCTCTTAACAATTCATGGCATTTGACCGCATTTGCGGGGATTT 943
QY 1149 CCAGCAACCTGCACACAGTTGCTTGAGGAGCGCTCCATTTGCCGAGA---TCATCATCAACA 1205
DB 944 TGAGACATCTTTTATGTTCTATGAGCGGATACCAAGTAGAAAAAGTGAATTTCTCATC 1003
QY 1206 GCAATTACCGATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1265
DB 1004 CAAATTATGACTCCAAAGACCAAGAAACAATGATGATGATGATGATGATGATGATGATG 1063
QY 1266 TGACCTGTCGCTCAGATCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1325
DB 1064 TGACTTTCAACGACCTAGTGAACCAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
QY 1326 TCAATGAGACCTGCTGATCAGGCTTTGGCAAGACCAAGGAGAGACAGATGACAAGACAT 1385
DB 1124 CAGAACAGCTCTGCTGGATTTCCGGTGGGGGGCCACCGAGAGA---AAGGAGAGACCT 1180
QY 1386 CCCCCTTCCTCCGGAGGTGAGTCAATCTCATGACTTCAAGAAATGCAATGACTACT 1445
DB 1181 CAGAAGTGTGAAAGCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
QY 1446 TGGTCTATGACAGTTACTTACCCCAAGGATGATGTGCTGGGACCTTCTGGGGGCA 1505
DB 1241 ATGTCTATGACAACTGATACACAGCATGATCTGTGCGGCTTCTGAGGGGAGCG 1300
QY 1506 GAGACTCTCTCCAGGAGAGAGCGGGGGCTTCTGTGTGAGCAGAAACAACTGCTGT 1565
DB 1301 TCGATTCTTCCAGGGTGACAGTGGAGGCTCTGTGCTCACTTCGAAGAAACAATATCTGGT 1360
QY 1566 ACCTGGAGGTGTACAGCTGGGCGACAGCTGTGGCAGAGAAACAACTGCTGT 1625
DB 1361 GGCTGATAGGGGATACAGCTGGGGTCTGCTGTGCAAGCTTACAGACAGGAGTGT 1420
QY 1626 ACACCAAGTACAGAGTCTTCTCCCTGATTTACAGCAAGATGAGAGCGAGG 1679

Ds 1421 ACGGAAATGATGGTATTCACGGACTGGATTTATCGACAATGAGGGCAGAGC 1474

RESULT 9
US-09-342-749-29
; Sequence 29, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-749-29

Query Match 10.0%; Score 175.6; DB 3; Length 2479;
Best Local Similarity 54.4%; Pred. No. 2.2e-34;
Matches 398; Conservative 0; Mismatches 328; Indels 6; Gaps 2;

QY 969 GGATCGTGGAGGGCGCTCGGATAGCAAGTGGCTTCGCAAGTGAGTCTGCACCT 1028
Ds 820 GGATCGTGGAGGGCGCTCGGAGCGCGCTCCCGGGGCGCTGGCCCTGGCAGGTGAGCTTGACG 879
QY 1029 TCGGCACCAACCCATCTGTGGAGGCAAGCTCTATGACGCCAGTGGTGTCTCACTGCCG 1088
Ds 880 TCCAGAACGTCCACGCTGTGGAGGCTCCATCATCCCCCGAGTGGATGTCGACAGCG 939
QY 1089 CCACCTGCTTCTTCGTGACCCGGGAGAGGTCTCTGAGGGCTGGAAGGTGTACGCGGCA 1148
Ds 940 CCACCTGCTGGAAGAACCTCTTAACAATCATGCGCATTTGACGCGCATTTGCGGGGATTT 999
QY 1149 CCAGCAACCTGCACGATTCCTTGAGCGAGCTCCATTCGCGAGA---TCATCATCAACA 1205
Ds 1000 TGAGACAATCTTTTATGTTCTATGGAGCGGATACCAAGTACAAAAGTATTTCTCATC 1059
QY 1206 GCAATTACACCGATGAGGAGGACGATGACATCGCCCTCATCGCGCTCTCCAAGCCCC 1265
Ds 1060 CAAATTATGACTCCAGAACCAAGAACAAATGACATTTGGCTGTATGAAGCTGCAGAGCCTC 1119
QY 1266 TGACCTGTCCGCTCATATCCACCTGCTTGCCTCCCGATGCGATGACAGACCTTTAGCC 1325
Ds 1120 TGACTTTCAACGACCTAGTGAAGAACCAAGTGTCTGCGCCAAACCCAGGCGATGATGTCGAGC 1179
QY 1326 TCAATGAGACCTGCTCGATCAGAGGCTTTGGCAAGACCCAGGGGAGACAGATGACAAGACAT 1385
Ds 1180 CAGAACAGCTCTGCTGATTTCCGGTGGGGGCGCCACCGAGGAGA---AAGGGAAGACCT 1236
QY 1386 CCCCCCTTCTCCGGAGGAGTGGAGTCAATCTCATTCGACTTCAAGAAATGCAATGACTACT 1445
Ds 1237 CAGAGTGTGAAACGCTGCGCAAGGTGCTTCTCAATTGAGACACAGAGATGCAACAGCAGAT 1296
QY 1446 TGGTCTATGACAGTTACCTTACCCCAAGGATGATGTCTGCGGGGACCTTCGTGGGGGCA 1505
Ds 1297 ATGTCTATGACAACCTGATCACAACCGACCATGATCTGTGCGGCTTCTGTCAGGGGAAACG 1356
QY 1506 GAGACTCTCCAGGGGAGACAGCGGGGGCTCTTGTGCTGTGAGCAGAACAAACCGCTGCT 1565
Ds 1357 TCGATTCTTCCAGGGTGAAGTGGAGGGCTCTGTGCTCACTTCAACAAACAATATCTGGT 1416
QY 1566 ACTTGCAGGTGTCAACAGCTGGGGCAGACGGCTGTGGCCAGAGAAACAAACCTGGTGTGT 1625
Ds 1417 GGCTGATAGGGGATACAAGCTGGGGTCTGCTGTGCGCAAGCTTACAGACCAAGGAGTGT 1476

QY 1626 ACACCAAGTGCACAGAGTCTTCCCTGATTTTACAGCAGATGGAGCGAGGTGGAT 1685
Ds 1477 ACGGAAATGATGGTATTCACGGACTGGATTTATCGACAATGAGGGCAACCGGTAAT 1536
QY 1686 TCAGAAAATCCT 1697
Ds 1537 CCATATGGTCTT 1548

RESULT 10
US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-840-29

Query Match 10.0%; Score 175.6; DB 4; Length 2479;
Best Local Similarity 54.4%; Pred. No. 2.2e-34;
Matches 398; Conservative 0; Mismatches 328; Indels 6; Gaps 2;

QY 969 GGATCGTGGAGGGCGCTCGGATAGCAAGTGGCTTCGCAAGTGAGTCTGCACCT 1028
Ds 820 GGATCGTGGAGGGCGCTCGGAGCGCGCTCCCGGGGCGCTGGCCCTGGCAGGTGAGCTTGACG 879
QY 1029 TCGGCACCAACCCATCTGTGGAGGCAAGCTCTATGACGCCAGTGGTGTCTCACTGCCG 1088
Ds 880 TCCAGAACGTCCACGCTGTGGAGGCTCCATCATCCCCCGAGTGGATGTCGACAGCG 939
QY 1089 CCACCTGCTTCTTCGTGACCCGGGAGAGGTCTCTGAGGGCTGGAAGGTGTACGCGGCA 1148
Ds 940 CCACCTGCTGGAAGAACCTCTTAACAATCATGCGCATTTGACGCGCATTTGCGGGGATTT 999
QY 1149 CCAGCAACCTGCACGATTCCTTGAGCGAGCTCCATTCGCGAGA---TCATCATCAACA 1205
Ds 1000 TGAGACAATCTTTTATGTTCTATGGAGCGGATACCAAGTACAAAAGTATTTCTCATC 1059
QY 1206 GCAATTACACCGATGAGGAGGACGATGACATCGCCCTCATCGCGCTCTCCAAGCCCC 1265
Ds 1060 CAAATTATGACTCCAGAACCAAGAACAAATGACATTTGGCTGTATGAAGCTGCAGAGCCTC 1119
QY 1266 TGACCTGTCCGCTCATATCCACCTGCTTGCCTCCCGATGCGATGACAGACCTTTAGCC 1325
Ds 1120 TGACTTTCAACGACCTAGTGAAGAACCAAGTGTCTGCGCCAAACCCAGGCGATGATGTCGAGC 1179
QY 1326 TCAATGAGACCTGCTCGATCAGAGGCTTTGGCAAGACCCAGGGGAGACAGATGACAAGACAT 1385
Ds 1180 CAGAACAGCTCTGCTGATTTCCGGTGGGGGCGCCACCGAGGAGA---AAGGGAAGACCT 1236
QY 1386 CCCCCCTTCTCCGGAGGAGTGGAGTCAATCTCATTCGACTTCAAGAAATGCAATGACTACT 1445
Ds 1237 CAGAGTGTGAAACGCTGCGCAAGGTGCTTCTCAATTGAGACACAGAGATGCAACAGCAGAT 1296
QY 1446 TGGTCTATGACAGTTACCTTACCCCAAGGATGATGTCTGCGGGGACCTTCGTGGGGGCA 1505

Db 1297 ATGTCTATGACAAACCTGATCACACACAGCCATGATCTGTGCCGGCTTCTTCGACGGGAACG 1356
 QY 1506 GAGACTCTCCAGGAGAGACAGCGGGGGCTCTTGTCTGTGAGCAGAACACACCGCTGGT 1565
 Db 1357 TCATCTTCCAGAGGTGACAGTGGAGGGCTCTGTCTATCTTGAACAAATATCTGGT 1416
 QY 1566 ACCTGGCAGGTGTACACAGCTGGGGCAAGGCTGTGGCCAGAGAAACAAACCTGGTGTGT 1625
 Db 1417 GGCTGATAGGGATACAAAGCTGGGGTCTGGCTGTGCCAAAGCTTACAGACCAAGAGTGT 1476
 QY 1626 ACACCAAGTGTACAGAAAGTCTTCCCTGGATTTACAGACAGATGAGAGCGAGTGGAT 1685
 Db 1477 ACGGGAATGTGATGTGATTCACCGACTGGATTTATCGACAAATGAAGGCCAAACGGCTAAT 1536
 QY 1686 TCAGAAATCT 1697
 Db 1537 CCACATGGTCTT 1548

RESULT 11
 US-09-261-416-1
 ; Sequence 1, Application US/09261416A
 ; Patent No. 6291663
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; APPLICANT: Underwood, Lowell J.
 ; TITLE OF INVENTION: TADG-12 J. No. 6291663el Transmembrane Serine Protease
 ; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
 ; FILE REFERENCE: D6192
 ; CURRENT APPLICATION NUMBER: US/09/261,416A
 ; CURRENT FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO 1
 ; LENGTH: 2416
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; LOCATION: 144..1511
 ; OTHER INFORMATION: CDS
 US-09-261-416-1

Query Match 9.1%; Score 158.2; DB 3; Length 2416;
 Best Local Similarity 55.4%; Pred. No. 4.8e-30;
 Matches 414; Conservative 0; Mismatches 318; Indels 15; Gaps 5;
 QY 953 AGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCCTTGG 1012
 Db 777 AGGGCTACAGCTCAGCGCATCGTGGGTGAAACATGTCCTTGTCTCGCAGTGGCCCTGG 836
 QY 1013 CAAGTGTGCTGACTTGGGACCAACCCACATCTGTGGAGGACGCTCATTTGACGCCCGAG 1072
 Db 837 CAGGCCAGCCTTCAGTTCAGGGCTACACCTGTGCGGGGGCTCTGTCTATCACGCCCTGT 896
 QY 1073 TGGTGTCTCACTCGCGGCCACTGTCTTCTGTGACCGCGGAGAGGTCCTGGAGGGCTGG 1132
 Db 897 TGGATCATCATCTGTGACACATGTGTTATG-----ACTTGTACTTCCCAAGTCATGG 950
 QY 1133 AAGGTGTAGCGGGGACCCAGCAACCTGCACAGTTGCTGTGAGGAGCCTTCCATGGCCGAG 1192
 Db 951 ACCATCCAGTGGGTCTAGTTTCCCTGTGTGACAAATCCAGCCCCATCCACTTGTGTGGAG 1010
 QY 1193 ATCATCAT---CAACAGCAATTTACCCGATGAGGAGGACGACTATGACATGCCCTCATG 1249
 Db 1011 AAGATTGTTTACCAAGCAAGTACCAAGCCAAAGAGGCTGGGCAATGATCATGCCCTTATG 1070
 QY 1250 CGGTGTCCAAAGCCCCCTGACCTGTGCTGCTACATCCACCTGTGCTTCCCTCATGCTAT 1309
 Db 1071 AAGTGGCGGGGCACTCAGCTTCAATGAATGATCCAGCTGTGTGCTGCTGCCCACTCT 1130
 QY 1310 GGACAGACCTTTCAGCTCAATGAGACCTGTGATGATCAGAGCTTTGGCAAGCCAGGAG 1369
 Db 1131 GAAGAGAACTTCCCGGATGGAAGAGTGTGCTGAGCTCAGGATGGGGGGCCACAGAGGAT 1190

QY 1370 ACAGATGACAAAGACATCCCCCTTCTCTCGGGAGGTGCAAGTCAATCTCATGACTTC-AA 1428
 Db 1191 GGAGGTGAC---GCCCTCCCCCTCTCTGAACACACCGCGGCCCTCCCTTTGATTTCCAAACA 1247
 QY 1429 GAATGCAATGACTACTTGTCTATGACAGTTACTTACCCCAAGAGTATGATGTGCTGG 1488
 Db 1248 GATCTGCAACCAACAGGACGTGTACCGTGGCATCACTCTCCCTCCATGCTCTGCGGGG 1307
 QY 1489 GGAACCTTCTGTGGGGG---AGAGACTCTCTGCGGAGACAGCGGGGGGCTCTTGTCTGT 1546
 Db 1308 CTACTTGAACGGGTGGGTTGGAACACAGCTGCGAGGGGACAGCGGGGGGCCCTGCTGTGT 1367
 QY 1547 GAGAGAACAAACCGCTGTGTACCTGGCAGGTGTACAGCTGGGGGACAGGCTGTGGCCAG 1606
 Db 1368 CAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAAGCTTTGGCATCGGCTGCGCAGAC 1427
 QY 1607 AGAAACAAACCTGTGTGTACACCAAGATGACAGAGTCTTCTCCCTGGATTTACAGCAAG 1666
 Db 1428 GTGAACCAAGCCTGGGGGTGTACACCCGTGTCACTCTTCTGGACTGGATCCAGAGCAG 1487
 QY 1667 ATGGAGAGCGAGGTGCGATTTCAGAAAA 1693
 Db 1488 ATGGAGAGAGACCTAAAAACCTGAAGA 1514

RESULT 12
 US-09-518-046-3
 ; Sequence 3, Application US/09518046
 ; Patent No. 6294663
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Brien, Timothy J.
 ; APPLICANT: Underwood, Lowell J.
 ; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
 ; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
 ; FILE REFERENCE: D6192CIP
 ; CURRENT APPLICATION NUMBER: US/09/518,046
 ; CURRENT FILING DATE: 2000-03-02
 ; EARLIER APPLICATION NUMBER: 09/261,416
 ; EARLIER FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 3
 ; LENGTH: 2544
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
 US-09-518-046-3

Query Match 8.8%; Score 154.2; DB 3; Length 2544;
 Best Local Similarity 58.1%; Pred. No. 4.9e-29;
 Matches 292; Conservative 0; Mismatches 208; Indels 3; Gaps 1;
 QY 1191 AGATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATGCCCTCATGC 1250
 Db 1143 AGATTGTCTACACAGCAAGTATCAAGCCAAAGAGCTGGGCAATGACATGCCCTTATGA 1202
 QY 1251 GGCTGTCCAAAGCCCCCTGACCTGTCCGCTCACTCCACCCCTGCTTGTGCTCCCCATGCA 1310
 Db 1203 AGCTGGCGGGCCACTCAGGTTCAATGAATGATCCAGCCTGTGTGCTGCCCACTCTG 1262
 QY 1311 GACAGACTTTAGCCTCAATGAGACCTGTGTGATCAAGGCTTTGGCAAGACGAGGAGA 1370
 Db 1263 AAGAGAACTTCCCGATGGAAGTGTCTGAGCTCAGGATGGGGGGCCACAGAGGATG 1322
 QY 1371 CAGATGACAAAGACATCCCCCTTCTCCGGAGGTGACGCTCAATCTCATGACTTTCAAGA 1430
 Db 1323 GAGGTGAC---GCCCTCCCCCTGTCTGAAACACAGCGGGCGCTCCCTTTGATTTCCAAACA 1379
 QY 1431 AATGCAATGACTACTTGTCTATGACAGTTTACCTTTACCCCAAGGATGATGTGTGCTGGGG 1490
 Db 1380 TCTGCAACCAACAGGAGCGTGTACGGTGGCATCATCTCCCTCCCTCCATGCTCTGCGGGCT 1439

QY 1491 ACCTTGTGGGCGAGAGACTCTGCGGAGAGACAGGGGGGCTCTTGTCTGTGAGC 1550
Db 1440 ACTGACGGGTGGCGTGAGCAGCTGCGGAGGAGACAGCGGGGGGCTCTGTTGTCAAG 1499
QY 1551 AGAACAAACCGCTGTGTACCTGGCAGGTGTACACAGCTGGGCGACAGGGCTGTGGCCAGAGAA 1610
Db 1500 AGAGGAGGCTGTGGAGTTAGTGGAGCGACAGCTTTGGCATCGGCTGGCGAGAGTGA 1559
QY 1611 ACAAACCTGTGTGTACACCAAGATGACAGAACTTCTTCCCTGGATTTACAGCAAGATGG 1670
Db 1560 ACAAGCCTGGGGTGTACACCGGTGTACCTCTTCTCGAGCTGTGATCCACGAGCATGG 1619
QY 1671 AGAGCGAGGTGCGATTGAGAAA 1693
Db 1620 AGAGAGACCTAAAAACCTGAAGA 1642

RESULT 13

US-09-510-738A-188
; Sequence 188, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length cDNA of hepsin
US-09-510-738A-188

Query Match 8.5%; Score 148.4; DB 3; Length 1783;
Best Local Similarity 53.3%; Pred. No. 1.2e-27;
Matches 448; Conservative 0; Mismatches 356; Indels 36; Gaps 5;

QY 867 ACACCTCCACCATCCAGGAAGCTCCACAGGTCTGATGCTTCCAGCGGTATATCT 926
Db 625 ACACCGAGGCTGCTGGAGTCTATCTCCGTGTGATTTGCCCGCAGAGCGCTTCTTGG 684
QY 927 CCTCCAGTGTTCCTCCACTCGGAGTCTGAGGCGCATGACCGGG---CGGATCGTGGAGGGG 983
Db 685 CCGCATCTGCCAAGACTGTGGCGCAGAGCTGCGCGTGGACCGCATCTGGAGGCC 744
QY 984 CGTGGCCTCGGATAGCAAGTGGCTTGGCAAGTGTGCACTTGGCACCACCCACA 1043
Db 745 GGGACACCAAGCTTGGGCGGCTGGCGGAGTCTGATGATGAGGACACACC 804
QY 1044 TCTGTGGAGCAGCTATTGACGCCAGTGGTGTCTCATCTGCGGCCCTCTTC--- 1099
Db 805 TCTGTGGGATCTCTGCTCTCGGAGCTGGGTGTGACAGCGGCCCTCTTCCCG 864
QY 1100 -----TTCTGTGACCCGGAGAGGTCTCTGGAGGCTGGAAGGTGTAGCGGGCA 1148
Db 865 AGCGGAACCGGTCTCTCCGATGGCGAGTGTTCGGGTGCGGTGGCCAGGCTCTC 924
QY 1149 CAGCAACCTGACAGTGTGCTGAGGAGCAGCTTCATTTGGCGGAGATCATCAACAGCA 1208
Db 925 CCGAGGTCTGACGTGGGGGTGACAGCTGTGTCTTACCAAGGGGCTATCTTCCCTTC 984
QY 1209 ATTACACCGAT---GAGGAGAGCTATGACATCGCCCTCATCTGCGGTCTCAAGCCC 1265
Db 985 GGGACCCCAACAGCGAGGAGACAGCAACATATGCTCTGGTCTCACTCTCCAGTCCCC 1044
QY 1266 TGACCTCTGCTGCATCATCCACCTGCTGCTCCCATGTCATGACAGACCTTTAGCC 1325

Db 1045 TGGCCCTCAGAGATATCATCCAGCTGTGTGCTCCAGCTGCGGCGAGGCCCTGTGTGG 1104
QY 1326 TCAATGAGACTCTGTGATCAGAGGCTTTGGCAAGACCCAGGAGACAGATGCAAGACAT 1385
Db 1105 ATGCGAAGATCTGTACCGTACCGGCTGGGGCAA---CAGCAGTACTATGGCCAAACAGG 1161
QY 1386 CCCCCTTCTCCCGGAGGTGCAGGTCTCATCTCATGCACTTCAAGAAATGCATGACTACT 1445
Db 1162 CCGGGGTACTCCAGGAGGCTCGAGTCTCCCAATATCAGCAATCATGTCTGCAATGGCGCTG 1221
QY 1446 TGGTCTATGACAGTTACTTACCCCAAGAGTGTGTCTGCTGGGAGCTTCTGTTGGGCA 1505
Db 1222 ACTTCTATGGAACACCATGACGCCAAGATTTCTGTCTGTGTACCCGAGGGTGGCA 1281
QY 1506 GAGACTCTCCCGGAGGAGACAGCGGGGGGCTCTTGTCTGTGACAGAACAAAC----- 1558
Db 1282 TTGATGCTCTGCCAGGGCGACAGCGGTGTCCTTTGTGTGTGAGGACAGCATCTCTCGGA 1341
QY 1559 -----CGCTGTACTCTGGCAGGTGTACAGCTGGGGCACAGGCTGTGGCCAGAGAACA 1613
Db 1342 CGCCACGTTGGCGGCTGTGTGGCAATTGTGAGTTGGGGCACTGGCTGTGCCCTGCCCAGA 1401
QY 1614 AACTGTGTGTACACCAAGTGCAGAGTCTTCTCCCTGATTTACAGCAAGATGAGA 1673
Db 1402 AGCAGCGCTACACCAAGTCACTGACTTCCGGAGTGTGATCTTCCAGGCCATAAGA 1461

RESULT 14

US-09-861-966-188
; Sequence 188, Application US/09861966
; Patent No. 8518028
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A/Div
; CURRENT APPLICATION NUMBER: US/09/861,966
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 09/510,738
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length cDNA of hepsin
US-09-861-966-188

Query Match 8.5%; Score 148.4; DB 4; Length 1783;
Best Local Similarity 53.3%; Pred. No. 1.2e-27;
Matches 448; Conservative 0; Mismatches 356; Indels 36; Gaps 5;

QY 867 ACACCTCCACCATCCAGGAAGCTCCACAGGTCTGATGCTTCCAGCGGTATATCT 926
Db 625 ACACCGAGGCTGCTGGAGTCTATCTCCGTGTGATTTGCCCGCAGAGCGCTTCTTGG 684
QY 927 CCTCCAGTGTTCCTCCACTCGGAGTCTGAGGCGCATGACCGGG---CGGATCGTGGAGGGG 983
Db 685 CCGCATCTGCCAAGACTGTGGCGCAGAGTGTCCCGTGGACCGCATCTGGAGGCC 744
QY 984 CGTGGCCTCGGATAGCAAGTGGCTTGGCAAGTGTGCACTTGGGCAACACCCACA 1043
Db 745 GGGACACCAAGCTTGGGCGGCTGGCGCAGAGTGTCCCGTGGACCGCATCTGGAGGCC 804
QY 1044 TCTGTGGAGCAGCTCATTTGACGCCAGTGGTGTCTCATCTGCGGCCCTCTTC--- 1099
Db 805 TCTGTGGGATCTCTGCTCTCCGGGACTGGGTGTGACAGCGGCCCTCTTCCCGG 864
QY 1100 -----TTCTGTGACCCGGAGAGCTCTCTGAGGCTGGAAGGTGTACCGGGCA 1148
Db 865 AGCGGAACCGGTCTCTGTCCGATGCGAGTGTTCCTCCGTGCGGTGGCCAGGCTCTC 924

1149 CCAGCAACCTGCGACCAAGTTGCTGAGGCGAGCCCTCCATTGCGGAGATCATCATCAACAGCA 1208
Db 925 CCCAAGCTCTGAGCTGGGGGTGAGGCTGTGCTTACCAAGGGGGTATCTTCCCTTTC 984
1209 ATTACACCGAT---GAGGAGGACGACTATGACATGCGCCCTCATGCGGCTGTCCAGGCC 1265
Db 985 GGGACCCCAACAGCGAGGAGAAAGCAACGATATGCGCTTGGTCCACCTCTCCAGTCCCC 1044
1266 TGACCTGTCTCGCTCATCATCCACCTGCTTGGCTCCCATGTCATGAGACACCTTTAGCC 1325
Db 1045 TGCCCTTCAAGATATCATCCAGCTGTGTGCTCCAGCTGCGGCGAGGCCCTGTGG 1104
1326 TCAATGAGACTGCTGATCAGAGCTTTGGAGAACCCAGGAGACAGATGACAGACAT 1385
Db 1105 ATGCAAGATCTGTACCGTACCGGCTGGGGGCAA---CACGCACTATATGCGCAACAGG 1161
1386 CCCCCTTCTCCGGGAGTCAAGTCAATCTCATGACTTCAAGAAATGCAATGACTACT 1445
Db 1162 CCGGGGTACTCCAGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCCGTG 1221
1446 TGCTCTATGACAGTTACTTACCCCAAGAGTGTGTGCTGGGGACCTTCTGGGGGCA 1505
Db 1222 ACTTCTATGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCA 1281
1506 GAGACTCTGCGAGGAGACAGCGGGGGCTCTTGTCTGTGAGCAGCAAC--- 1558
Db 1282 TTGATGCTGCGAGGGGACAGCGGGTGTCTTGTGTGTGAGGACAGCATCTCTCGGA 1341
1559 -----CGCTGTACTCGAGGTGTACCCAGTGGGGCAGAGGCTGTGGCCAGAGAAACA 1613
Db 1342 CGCCACGTTGGCGCTGTGTGGCAATTGTGAGTTGGGCACTGGCTGTGCTGGCCAGA 1401
1614 AACCTGTGTGTACCAAAAGTGCAGAGTTCTTCCCTGGATTTCAGCAAGATGAGA 1673
Db 1402 AGCCAGGCGTCTACCAAAAGTGCAGTGTCTCCGGAGTGGATCTTCAGGCCATAAGA 1461
RESULT 15
US-09-742-703-3
; Sequence 3, Application US/09742703
; Patent No. 6423543
; GENERAL INFORMATION:
; APPLICANT: Patrick Allen Marcotte
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEP5IN EXPRESSION
; FILE REFERENCE: RTS-0090
; CURRENT APPLICATION NUMBER: US/09/742,703
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (826)..(2079)
US-09-742-703-3
Query Match 8.5%; Score 148.4; DB 4; Length 2363;
Best Local Similarity 53.3%; Pred. No. 1.3e-27;
Matches 448; Conservative 0; Mismatches 356; Indels 36; Gaps 5;
Qy 867 ACAACTCCACCATCCAGAAAGCTTCCAGAGTCTGAATGCTTCCAGCGGTATATCT 926
Db 1205 ACACCCAGAGGCTGTGAGGCTCATCTCCGTGTGTGATTGCCCCCAGAGGCGGTTTCTGG 1264
Qy 927 CCCTCCAGTGTCCACATCGGAGCTGAGGCCATGACCGGG---CGGATCGTGGAGGGG 983
Db 1265 CGGCATCTGCCAAGACTGTGGCCCGCAGAGAGCTCCCGTGGACCGCATCTGTGGAGGCC 1324
Qy 984 CGCTGGCTCGGATAGCAAGTGGCCCTTGGCAAGTGAATGCTGCACTTTCGCCACCAACCCACA 1043
Db 1325 GGGACACCAAGTGGGCCCGGTGGCGGTGGCAAGTGGCAAGTTCGCTATGATGGAGCACACC 1384

1044 TCTGTGAGGCGAGCTCATTTGACGCCCAAGTGGTGTCTCACTGCGGCCCACTGCTTC----- 1099
Db 1385 TCTGTGGGGGATCCCTGCTCTCCGGGGACTGGGTGCTGACAGCCGCCCACTGCTTCCCGG 1444
Qy 1100 -----TTCTGTGACCCCGGGAGAGGTCTCTGAGGGCTGGAAAGGTGTACGCGGGCA 1148
Db 1445 AGCGGAACCGGGTCTTGTCCCGATGCGAGTGTGTCGCGGTGCGGTGGCCAGGCTCTC 1504
Qy 1149 CCAGCAACCTGCAACCAAGTTGCTGAGGCGAGCCCTCCATTGCGGAGATCATCATCAACAGCA 1208
Db 1505 CCACAGGTCTGAGCTGGGGGTGCGAGCTGTGCTTACCAAGCGGGGTATCTTCCCTTTC 1564
1209 ATTACACCGAT---GAGGAGGACGACTATGACATGCGCCCTCATGCGGCTGTCCAGGCC 1265
Db 1565 GGGACCCCAACAGCGAGGAGAAAGCAACGATATGCGCTTGGTCCACCTCTCCAGTCCCC 1624
1266 TGACCTGTCTCGCTCATCATCCACCTGCTTGGCTCCCATGTCATGAGCAGACCTTTAGCC 1325
Db 1625 TGCCCTTCAAGATATCATCCAGCTGTGTGCTTCCAGCTGCGGCGAGGCCCTGTGG 1684
Qy 1326 TCAATGAGACTGCTGATCAGAGGCTTTGGCAAGACCCAGGAGACAGATGACAGACAT 1385
Db 1685 ATGCAAGATCTGTACCGTGCAGCGGCTGGGGCAA---CACGCACTATATGCGCAACAGG 1741
1386 CCCCCTTCTCCGGGAGTGCAGGTCAATCTCATGACTTCAAGAAATGCAATGACTACT 1445
Db 1742 CCGGGGTACTTCCAGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCCGTG 1801
Qy 1446 TGCTCTATGACAGTTACTTACCCCAAGAGTGTGTGCTGGGGACCTTCTGGGGGCA 1505
Db 1802 ACTTCTATGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCA 1861
1506 GAGACTCTGCGAGGAGACAGCGGGGGCTCTTGTCTGTGAGCAGCAAC----- 1558
Db 1862 TTGATGCTGCGAGGGGACAGCGGGTGTCTTGTGTGTGAGGACAGCATCTCTCGGA 1921
Qy 1559 -----CGCTGTACTGCGAGGTGTACAGCTGGGGCAGAGGCTGTGGCCAGAGAAACA 1613
Db 1922 CGCCACGTTGGCGCTGTGTGGCAATTGTGAGTTGGGGCACTGGCTGTGCTGGCCCGAGA 1981
Qy 1614 AACCTGTGTGTACCAAAAGTGCAGAGTTCTTCCCTGGATTTCAGCAAGATGAGA 1673
Db 1982 AGCCAGGCGTCTACCAAAAGTGCAGTGTCTCCGGAGTGGATCTTCCAGGCCATAAGA 2041

Search completed: December 17, 2003, 20:21:56
Job time : 136 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 17, 2003, 20:22:02 ; Search time 457 Seconds

(without alignments)
4097.808 Million cell updates/sec

Title: US-09-879-792-12

Perfect score: 2999

Sequence: 1 MERDSHGNASPARTPSAGAS.....TEVLPWYISXMSREVRFRKS 562

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched:

2211378 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2_1/USPTO.spool_p/US09879792/runat_17122003_164702_50/app_query.fasta_1.711
-DB=Published Applications NA -QFMT=fastap -SUFFIX=decl17.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blowsum2
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=ptc -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09879792 @CGN 1 1 85 @runat 17122003_164702_50
-NCFU=6 -ICFU=3 -NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgm2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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4: /cgm2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	2999	100.0	1748	9	US-09-879-792-11	Sequence 11, Appl
2	2956	98.6	2393	13	US-10-353-690-99	Sequence 99, Appl
3	2775.5	92.5	1614	9	US-09-888-615-45	Sequence 1, Appl
4	2291.5	76.4	1434	15	US-10-177-661-1	Sequence 14, Appl
5	2287	76.3	1314	11	US-09-898-837A-14	Sequence 17, Appl
6	2287	76.3	1314	11	US-09-898-837A-17	Sequence 3, Appl
7	2108	70.3	1341	15	US-10-177-661-3	Sequence 16, Appl
8	1869	62.3	1078	11	US-09-898-837A-16	Sequence 35, Appl
9	1855	61.9	1230	9	US-09-879-792-35	Sequence 5, Appl
10	1436	47.9	1222	9	US-09-804-156-5	Sequence 3, Appl
11	1436	47.9	1222	13	US-10-319-519-5	Sequence 5, Appl
12	1436	47.9	1222	13	US-10-125-459-3	Sequence 5, Appl
13	1436	47.9	1222	14	US-10-067-761-5	Sequence 28, Appl
14	1282.5	42.8	834	9	US-09-879-792-28	Sequence 30, Appl
15	893	29.8	678	9	US-09-879-792-30	Sequence 33, Appl
16	845.5	28.2	614	9	US-09-879-792-33	Sequence 6, Appl
17	785.5	26.2	3298	15	US-10-235-699-6	Sequence 22, Appl
18	745.5	24.9	2486	10	US-09-981-353-22	Sequence 5, Appl
19	743	24.8	3244	13	US-10-334-038-5	Sequence 929, App
20	743	24.8	3245	9	US-09-759-143-929	Sequence 929, App
21	743	24.8	3245	9	US-09-822-827-929	Sequence 929, App
22	743	24.8	3245	10	US-09-895-793-929	Sequence 929, App
23	743	24.8	3245	10	US-09-895-814-929	Sequence 929, App
24	743	24.8	3245	13	US-10-144-678A-929	Sequence 929, App
25	743	24.8	3245	13	US-10-294-025-929	Sequence 929, App
26	743	24.8	3245	14	US-10-012-896-929	Sequence 931, App
27	743	24.8	3245	9	US-09-759-143-931	Sequence 931, App
28	741.5	24.7	1476	9	US-09-780-669-931	Sequence 931, App
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31	741.5	24.7	1476	10	US-09-895-814-931	Sequence 931, App
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33	741.5	24.7	1476	13	US-10-294-025-931	Sequence 931, App
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38	741.5	24.7	1479	10	US-09-895-793-930	Sequence 930, App
39	741.5	24.7	1479	10	US-09-895-814-930	Sequence 930, App
40	741.5	24.7	1479	13	US-10-144-678A-930	Sequence 930, App
41	741.5	24.7	1479	13	US-10-294-025-930	Sequence 930, App
42	741.5	24.7	1479	14	US-10-012-896-930	Sequence 11, Appl
43	741.5	24.7	1479	14	US-09-776-191-11	
44	741.5	24.7	1656	11		
45	741.5	24.7				

ALIGNMENTS

RESULT 1
US-09-879-792-11
; Sequence 11, Application US/09879792
; Patent No. US20020061850A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; APPLICANT: Gedrich, Richard
; TITLE OF INVENTION: Regulation of Human Transmembrane Serine
; TITLE OF INVENTION: Protease
; FILE REFERENCE: 02973.00035
; CURRENT APPLICATION NUMBER: US/09/879,792
; CURRENT FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/211,224
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,353
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1748

; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
 ; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
 ; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
 ; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
 ; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
 ; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
 ; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules

; FILE REFERENCE: MP102-018P1RNOMIN
 ; CURRENT APPLICATION NUMBER: US/10/353,690

; CURRENT FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 60/353,224

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/364,529

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: 60/373,861

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/376,287

; PRIOR FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: 60/388,080

; PRIOR FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: 60/390,971

; PRIOR FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: 60/394,130

; PRIOR FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: 60/394,797

; PRIOR FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: 60/404,904

; PRIOR FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: 60/405,450

; PRIOR FILING DATE: 2002-08-23

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 99

; LENGTH: 2393

; TYPE: DNA

; ORGANISM: Homo Sapiens

; US-10-353-690-99

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Score:	2956.00	Matches:	553
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.82%	Mismatches:	0
Query Match:	98.57%	Indels:	0
DB:	13	Gaps:	0

US-09-879-792-12 (1-562) x US-10-353-690-99 (1-2393)

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Db	148	CCAGCCAGGCAATCTCCAGCTGGGACACTCCAGCCCGGGCATCTCCAGCCAGGCAATCT	207
Qy	41	ProAlaGlnAlaSerProAlaGlyThrProProGlyArgAlaSerProAlaGlnAlaSer	60
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Qy	61	ProAlaGlyThrProProGlyArgAlaSerProGlyArgAlaSerProAlaGlnAlaSer	80
Db	268	CCAGCTGGTATACCTCCAGCCCGGGCATCTCCAGCCCGGGCATCTCCAGCCAGGCAATCT	327
Qy	81	ProAlaArgAlaSerProAlaGlnAlaSerLeuSerArgSerSerGlyArgSerSer	100
Db	328	CCAGCCCGGGCAATCTCCAGCTGGGCACTTCCTCAGGTCCTCATCCGCGAGGTCATCA	387
Qy	101	SerAlaArgSerAlaSerValThrThrSerProThrArgValThrLeuValArgAlaThr	120
Db	388	TCCGCCAGGTCAGGCTCGGTGACAACTCCCAACACAGAGTGATACCTTGTGTAGACAAACA	447

Qy	121	ProValGlyAlaValProIleArgSerSerProIleArgSerAlaProAlaThrArgAla	140
Db	448	CCAGTGGGGGCTGTACCATCCGATCATCTCTCCAGGTGAGCAGCAGCAGCAGCAGCAGC	507
Qy	141	ThrArgGluSerProGlyThrSerLeuProIleArgSerThrTrpArgGlyGlyGlnGln	160
Db	508	ACAGGGAGAGCCCGAGTACGAGCTGCGGAGTTCACCTGCGGGAGGCGCAGAGCAG	567
Qy	161	LeuProIleGlyCysValLeuLeuLeuLeuAlaLeuValValSerLeuLeuLeu	180
Db	568	CTACCGCTCATCGGGTGGTCTCTCTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	627
Qy	181	PheGlnPheTrpGlnGlyHisThrGlyLeuArgTrpGlyGlnGlnGlnGlnGlnGlnGln	200
Db	628	TTCCAGTTCTGGCAGGGCCACACAGGATCAGGACAGGAGCAGGAGGAGGAGGAGGAGG	687
Qy	201	LeuHisAlaValArgCysAspGlyValValAspCysValLeuLeuLeuLeuLeuGly	220
Db	588	AGCAGCTGTCTGCTGTGACGGGTGGTGGATCTGCAAGCTGAAGAGTGAAGAGTGGGC	747
Qy	221	CysValArgPheAspTrpAspLysSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	240
Db	748	TGCGTGAAGTTGACTGGGACAGTCTCTGCTTAAATCTACTCTGCTGCTGCTGCTGCTGCT	807
Qy	241	TrpLeuProIleCysSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer	260
Db	808	TGGCTTCCCATCTGTAGCAGCAGCAGTGGATCTGCTTACTCTGAGAGAGCAGCAGCAGC	867
Qy	261	LeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaAsnSer	280
Db	868	CTGGTTTCGAGAGTGTCTACCGCAACCGAGGTGGCCACAGGATTTTGCACACAGC	927
Qy	281	PheSerLeuLeuArgTrpAsnSerThrIleGlnGlnSerLeuHisArgSerGluCysPro	300
Db	928	TTCTCAATCTTGAGATACCACTCCACCATCCAGGAAAGCCTCCACAGGTCTGAATGCCCT	987
Qy	301	SerGlnArgTrpIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThrGlyArg	320
Db	988	TCCAGCGGTATATCTCTCTCCAGTGTCCCACTCGGAGCTGAGGGGCTGAGGGGCTGAG	1047
Qy	321	IleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHisPhe	340
Db	1048	ATCGTGGAGGGGGCTGGCTCGGATAGCAGTGGCTTGGCAAGTGAAGTCTGCACTTC	1107
Qy	341	GlyThrThrHisIleCysGlyGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	360
Db	1108	GGCACCACCCACATCTGTGAGGAGCAGCTCATTCAGCCGCCAGTGGGTGCTCACTCCGCC	1167
Qy	361	HisCysPhePheValThrArgGluValLeuGluGlyTrpLysValTyrAlaGlyThr	380
Db	1168	CAGTCTTCTTCTGGTACCCCGGAGAGGTCTTGGAGGGCTGGAAGGTGTACCGGGGACC	1227
Qy	381	SerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleIleAsnSerAsn	400
Db	1228	AGCAACCTGACACGAGTTCCTTGGAGGAGCTCCATTCGAGATCATCATCAACAGCAAT	1287
Qy	401	TyrThrAspGluGluAspAspTrpAspIleAlaLeuMetArgLeuSerLysProLeuThr	420
Db	1288	TACACCGATGAGGAGGAGCAGTATGACATCGCCCTCATCGGCTGTCCAAAGCCCTGACC	1347
Qy	421	LeuSerAlaHisIleLeuProAlaCysLeuProMetHisGlyGlnThrPheSerLeuAsn	440
Db	1348	CTGTCCGCTCATCTCCACCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1407
Qy	441	GluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspAspLysThrSerPro	460
Db	1408	GAGACCTGCTGATCAGAGGTTTGGCAGACCGAGGAGCAGATGACAGACATCCCCC	1467
Qy	461	PheLeuArgGluValGlnValAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuVal	480
Db	1468	TTCTCTCGGAGGAGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGTGTC	1527
Qy	481	TyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGlyArgAsp	500

Db 1528 TATGACAGTTACCTTACCCCAAGCATGATGTGCTGGGAGACCTTGTGGGGCAGAGAC 1587
Qy 501 SerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAenAenArgTyrLeu 520
Db 1588 TCCTGCCAGGAGACAGCGGGGGGCTCTTGTGTGTGAGCAGAAACAACCGCTGGTACCTG 1647
Qy 521 AlaGlyValThrSerTyrGlyThrGlyCysGlnArgAenLysProGlyValTyrThr 540
Db 1648 GACAGTGTACACAGCTGGGGACAGCGCTGTGGCCAGAGAAACAACCTGTGTGTACACC 1707
Qy 541 LysValThrGluValLeuProTyrPheTyrSerLysMetGlu 554
Db 1708 AAGTGCAGACAGATTTCTTCCCTGGATTTACAGCAAGATGGAG 1749

RESULT 3

US-09-888-615-45
; Sequence 45, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CRENEPEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; PRIORITY FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-888-615-45

Alignment Scores:
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Score: 2775.50 Matches: 526
Percent Similarity: 91.96% Conservative: 0
Best Local Similarity: 91.96% Mismatches: 1
Query Match: 92.55% Indels: 45
DB: 9 Gaps: 2

US-09-879-792-12 (1-562) x US-09-888-615-45 (1-1614)

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Qy 21 ProAlaGlnAlaSerProAlaGlyThrProProGlyArgAlaSerProAlaGlnAlaSer 40
Db 61 CCAGCCCGAGGCATCTCCAGCTGGGACACCTCCAGCGCGGGCATCTCCAGCCCGAGGCATCT 120
Qy 41 ProAlaGlnAlaSerProAlaGlyThrProProGlyArgAlaSerProAlaGlnAlaSer 60
Db 121 CCAGCCCGAGGCATCTCCAGCTGGGACACCTCCAGCGCGGGCATCTCCAGCCCGAGGCATCT 180
Qy 61 ProAlaGlyThrProProGlyArgAlaSerProGlyArg 73
Db 181 CCAGCTGGTACACCTCCAGCGCGGGCATCTCCAGCGCGGGCATCTCCAGCCCGAGGCATCT 240
Qy 74 -----AlaSerProAlaGlnAlaSerProAlaArgAlaSerProAlaLeuAlaSer 90
Db 241 CCAGCCCGAGGCATCTCCAGCTGGGACACCTCCAGCGCGGGCATCTCCAGCCCGAGGCATCT 300
Qy 91 LeuSerArgSerSerGlyArgSerSerSerAlaArgSerAlaSerValThrThrSer 110
Db 301 CTTTCCAGGTCTCTATCCCGCAGGTATATATCCCGCAGGTCTCAGCCCTCGGTGACAACTCC 360

Qy 111 ProThrArgValTyrLeuValArgAlaThrProValGlyAlaValProIleArgSerSer 130
Db 361 CCAACCAAGTGTACCTTGTGTAGAGCAACCAAGTGGGGGCTGTACCCATCCGATCATCT 420
Qy 131 ProAlaArgSerAlaProAlaThrArgAlaThrArgGluSerProGlyThrSerLeuPro 150
Db 421 CCTGCCAGGTGAGCAGCAGCAACCAAGGCGCCACCAAGGAGAGCCCA ----- 465
Qy 151 LysPheThrTyrArgGluGlyGlnLysGlnLeuProLeuIleGlyCysValLeuLeuLeu 170
Db 465 ----- 465
Qy 171 IleAlaLeuValSerLeuIleLeuLeuPheGlnPheThrGlnGlyHisThrGlyIle 190
Db 466 -----GTCCAGTTCCTGGCAGGGCCACACAGGGATC 495
Qy 191 ArgTyrLysGluGlnArgGluSerCysProLysHisAlaValAlaValArgCysAspGlyValVal 210
Db 496 AGGTACAAGGAGCAGAGAGGAGAGCTGTCCCAAGCAAGCTGTTCGCTGTGACGGGGTGGG 555
Qy 211 AspCysLysLeuLysSerAspGluLeuGlyCysValArgPheAspTyrAspLysSerLeu 230
Db 556 GACTGCAAGCTGAGAGAGTGACGAGCTGGGCTGGGTGTGAGTGTGACTGGGACAAAGTCTCTG 615
Qy 231 LeuLysIleTyrSerGlySerHisGlnTyrLeuProIleCysSerSerAenTyrAen 250
Db 616 CTTAAATCTACTCTGGGTCTCCCATCAGTGGCTTCCCATCTGTAGCAGCAACTGGAAAT 675
Qy 251 AspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThr 270
Db 676 GACTCCTACTCAGAGAGACCTTCGCGAGCTGGGTTCGAGAGTGTCTCACCAGCAACC 735
Qy 271 GluValAlaHisArgAspPheAlaAenSerPheSerIleLeuArgTyrAenSerThrIle 290
Db 736 GAGGTGGCCCAAGGAGATTTTGGCAACAGCTTCTCAATCTTGAGATACAACTCCACCATC 795
Qy 291 GlnGluSerLeuHisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSer 310
Db 796 CAGGAAAGCCTCCACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTC 855
Qy 311 HisCysGlyValArgAlaMetThrGlyArgIleValGlyGlyAlaLeuAlaSerAspSer 330
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Qy 331 LysTyrProTyrGlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeu 350
Db 916 AAGTGGCTTGGCAAGTGAAGTCTGCACTTCGGCACCAACCAACATCTGTGGAGCAGCTC 975
Qy 351 IleAspAlaGlnTyrValLeuThrAlaAlaHisCysPhePheValThrArgGluLysVal 370
Db 976 ATTGACGCCAGTGGGTGCTCACTGCGGCCACTGTCTTCTGTGACCGGGAGAGGTC 1035
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Qy 391 SerIleAlaGluIleIleAenSerAenTyrThrAspGluGluAspTyrAspIle 410
Db 1096 TCCATTTGCGAGATCATCATCAACAGCAANTTACCGATGAGGAGGACGACTATGACATC 1155
Qy 411 AlaLeuMetArgLeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeu 430
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Qy 431 ProMetHisGlyGlnThrPheSerLeuAenGluThrCysTyrIleThrGlyPheGlyLys 450
Db 1216 CCAATGATGAGCAGACCTTTAGCTTCAATGAGACCTGTGTGATCAAGGCTTGGCAG 1275
Qy 451 ThrArgGluThrAspAspLysThrSerProPheLeuArgGluValGlnValAenLeuIle 470
Db 1276 ACCAGGAGACAGATGACAGACATCCCTTCTCCGGGAGGTGACAGGTCAATCTCATC 1335

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QY 471 AspPheLysCysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMet 490
Db 1336 GACTTCAAGAAATGCAATGACTACTTGGTCTATGACAGTTACCTTACCCCAAGATGATG 1395
QY 491 CysAlaGlyAspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeu 510
Db 1396 TGTGCTGGGACCTTCTGTGGGGCAGAGACTCTCTGCCAGGGAGACAGCGGGGCTCTT 1455
QY 511 ValCysGluGlnAsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrPdglyThrGlyCys 530
Db 1456 GTCTGTGAGCAGAAACCGCTGTGTCTGGCAGGTGTCAACAGCTGGGGCAGAGGCTGT 1515
QY 531 GlyGlnArgAsnLysProGlyValTyrThrLysValThrGluValLeuProTyrPileTyr 550
Db 1516 GGCAGAGAAACAAACCTGGTGTGTACACCAAGTGAAGAAAGTTCTTCCCTGGATTATC 1575
QY 551 SerLysMetGluSerGluValValArgPheArgLysSer 562
Db 1576 AGCAGATGGAGAGGAGTGTCCGATTCAAGAAATCC 1611

RESULT 4
US-10-177-661-1
; Sequence 1, Application US/10177661
; Publication No. US20030082783A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Virca, G. Duke
; TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE
; FILE REFERENCE: 3256-A
; CURRENT APPLICATION NUMBER: US/10/177,661
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/299,606
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1434)
; OTHER INFORMATION:
US-10-177-661-1

Alignment Scores:
Pred. No.: 9.94e-161 Length: 1434
Score: 2291.50 Matches: 424
Percent Similarity: 96.61% Conservative: 4
Best Local Similarity: 95.71% Mismatches: 12
Query Match: 76.41% Indels: 3
DB: 15 Gaps: 1

US-09-879-792-12 (1-562) x US-10-177-661-1 (1-1434)
QY 120 ThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThrArg 139
Db 112 TCCCCCACCCTCTCTCTGTCGAGCTCTCTCCAGCTCATATATTCCTTCCTGCTGCCGCC 171
QY 140 AlaThrArgGluSerProGlyThrSerLeuProLysPheThrTyrArgGluGlyGlnLys 159
Db 172 CTGCTCCTA-----GGTACGAGCTGCCAGGTTCACTGGCGGAGGGCCAGAG 222
QY 160 GlnLeuProLeuIleGlyCysValLeuLeuLeuLeuAlaLeuValSerLeuLeuIle 179
Db 223 CAGCTACCGCTCATCGGGTGGTGTCTCTCTCATTTGCTGGTGTTCGCTCATCATC 282
QY 180 LeuPheGlnPheTyrGlnGlyHisThrGlyLeuArgTyrLysGluGlnArgGluSerCys 199
Db 283 CTCCTCCAGTTCTTGGCAGGGCCACACAGGATCAGGTACAGGAGCAGAGGAGAGCTGT 342
QY 200 ProLysHisAlaValArgCysAspGlyValValAspCysLysLeuLysSerAspGluLeu 219
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Db 343 CCCAAGCAGCTGTTCTGCTGTGACGGGGTGGTGAAGCTCAAGCTGAAGAGTGAAGAGCTG 402
QY 220 GlyCysValArgPheAspTyrAspLysSerLeuLeuLysLysLysSerGlySerSerHis 239
Db 403 GCGTGGTGGAGTTTGAATGGGACAGTCTCTGCTTAAATCTACTCTCTGGGTCTCTCCCAT 462
QY 240 GlnTrpLeuProLysCysSerSerAsnTrpAsnAspSerTyrSerGluLysThrCysGln 259
Db 463 CAGTGGCTTCCCATCTGTAGCAGCACTGGGAATGACTCTTACTCAGAGAGACCTTGCACG 522
QY 260 GlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaAsn 279
Db 523 CAGCTGGGTTCAGAGTGTCTACCGGACCAACCGAGGTGGCCACAGGGATTTGGCCAC 582
QY 280 SerPheSerLeuLeuArgTyrAsnSerThrIleGlnGluSerLeuHisArgSerGluCys 299
Db 583 AGCTTCTCAATCTTGAATACAATCCACCATCCAGGAAAGCTCCACAGGTCTGAATGC 642
QY 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThrGly 319
Db 643 CTTTCCAGGGGTATATCTCTCCAGTGTTCCTGCTGCGGACTGAGGGCCATGACCGGG 702
QY 320 ArgIleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHis 339
Db 703 CGGATCGTGGAGGGGGCTGGCTCTGGATAGCAGTGGCTTGGCAAGTGAATCTGCAC 762
QY 340 PheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThrAla 359
Db 763 TTGGCACCACCCACATCTGTGGAGGACGCTCATTTGACGCCAGCTGGGTGCTCACTGCC 822
QY 360 AlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAlaGly 379
Db 823 GCCCACTGCTTCTTGTGACCCGGGAGAGGTCTCTGGAGGGCTGGAGGTGTACCGCGGC 882
QY 380 ThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleAsnSer 399
Db 883 ACCAGCAACCTGACACAGTTCCTGAGCGACCTCCATTGCGGAGATCATATCAACAGC 942
QY 400 AsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysProLeu 419
Db 943 AATTACACCGATGAGGAGGACGACTATGACATCGCTCATCGGCTGTCCAAGCCCTG 1002
QY 420 ThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSerLeu 439
Db 1003 ACCCTGTCCGCTCATCTCCACCTGCTTGCCTCCCATGCAATGCAAGACACCTTTAGCCTC 1062
QY 440 AsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspLysThrSer 459
Db 1063 AATGAGACCTCTGATCATCAGGCTTTGGCAAGACCGAGGAGACAGATGACAGACATCC 1122
QY 460 ProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyrLeu 479
Db 1123 CCTTCTCTCCGGAGGTGACAGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTG 1182
QY 480 ValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyLysArg 499
Db 1183 GTCTATGACATTTACCTTATCCCCAAGATGATGTGTCTGGGGACCTTCGTGGGGGCGAGA 1242
QY 500 AspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArgTrpTyr 519
Db 1243 GACTCTCCAGGAGGAGACAGCGGGGGGCTCTTGTCTGTAGAGAGACACACCGCTGGTAC 1302
QY 520 LeuAlaGlyValThrSerTrpGlyThrGlyCysGlnArgAsnLysProGlyValTyr 539
Db 1303 CTGGCAGGTGTCAACAGCTGGGGCAGAGCTGTGGCCAGAGAAACAAACCTGGTGTGTAC 1362
QY 540 ThrLysValThrGluValLeuProTyrPileTyrSerLysMetGluSerGluValArgPhe 559
Db 1363 ACCAAGTGAAGAAAGTTCTTCCCTGGATTTCAGCAGAGATGAGAGCGAGGTGCGATTTC 1422
QY 560 ArgLysSer 562
Db 1423 AGAAATCC 1431
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RESULT 5
US-09-898-837A-14
; Sequence 14, Application US/09898837A
; PUBLICATION INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spyttek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1263)
US-09-898-837A-14

Alignment Scores:
Pred. No.: 1,94e-160 Length: 1314
Score: 2287.00 Matches: 419
Percent Similarity: 99.76% Conservatives: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 76.26% Indels: 0
DB: 11 Gaps: 0

US-09-879-792-12 (1-562) x US-09-898-837A-14 (1-1314)

QY 143 GluSerProGlyThrSerLeuProLysPheThrTrpArgGluGlyGlnLysGlnLeuPro 162
DB 4 GAGAGCCAGGTACGAGCGCTGCCCAAGTTTCACCTGGCGGAGGCCGCAAGCAGCTACCG 63
QY 163 LeuLeGlyCysValLeuLeuLeuLeuAlaLeuValValSerLeuLeuLeuLeuPheGln 182
DB 64 CTCATCGGTGGTGGTCTCTCTCTCATGTGCCCTGGTGTTCGTCATCATCTCTTCCAG 123
QY 183 PheTrpGlnGlyHisThrGlyIleArgTyrLysGluGlnArgGluSerCysProLysHis 202
DB 124 TTCTGGCAGGGCCACACAGGATCAGTACAGGAGCAGAGGAGGAGGAGCTGTCCAGCAC 183
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QY 203 AlaValArgCysAspGlyValValAspCysLysLeuLysSerAspGluLeuGlyCysVal 222
DB 184 GCTGTTGCTGTGACGGGGTGGTGGACTGCAAGCTGCAAGAGTGAAGAGTGGGCTGGCTG 243
QY 223 ArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGlySerSerHisGlnTrpLeu 242
DB 244 AGGTTTGACTGGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTCCCATCAGTGGCTT 303
QY 243 ProIleCysSerSerAsnTrpAsnAspSerTyrSerGluLysThrCysGlnGlnLeuGly 262
DB 304 CCAATCTGTAGCAGCACTGGAACTGCTTACTCTCAGAGAGAGACTGCCAGCAGCTGGGT 363
QY 263 PheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaAsnSerPheSer 282
DB 364 TTCGAGAGTGTCTCACCGGACAAACGAGGTTGCCACAGGGATTTTGCACACAGCTTCTCA 423
QY 283 IleLeuArgTyrAsnSerThrIleGlnGlnSerLeuHisArgSerGluCysProSerGln 302
DB 424 ATCTTGAGATCAACTCCACCATCCAGGAAGGCTTCCACAGGTCTGAATGCCCTTCCAG 483
QY 303 ArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThrGlyArgIleVal 322
DB 484 CGGTATATCTCCCTCCAGTGTTCACACTGGGACTGAGGGCATGACCGGGCGGATCGTG 543
QY 323 GlyGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHisPheGlyThr 342
DB 544 GGAGGGCGCTGGCCTCGGATAGCAAGTGGGCTTGGCAAGTGAAGTCTGCATCTTCGGCAC 603
QY 343 ThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThrAlaAlaHisCys 362
DB 604 ACCCACATCTGTGGAGGCACGCTCATGACGCCAGTGGGTGCTCAGTGCGCCCACTGC 663
QY 363 PhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAlaGlyThrSerAsn 382
DB 664 TTCTTCGTGACCCGGGAGAGGTCTCTGAGAGGCTGGAAGGTGTACGCGGCACCAAC 723
QY 383 LeuHisGlnLeuProGluAlaAspIleAlaGluIleIleIleAsnSerAsnTyrThr 402
DB 724 CTGCACCAAGTTGCTTCAGGCGAGCTCCATTTGCCAGAGATCATCATCACAGCAATTACAC 783
QY 403 AspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysProLeuThrLeuSer 422
DB 784 GATGAGGAGGAGCAGCTATGACATCGCCTCATGCGGCTGTCCAGCCCTGACCCCTGTC 843
QY 423 AlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSerLeuAsnGluThr 442
DB 844 GCTCACATCCACCTTGCTTGCTCCCATGCATGCACAGACCTTTAGCCTCAATGAGACC 903
QY 443 CysTrpIleThrGlyPheGlyLysThrArgGluThrAspAspLysThrSerProPheLeu 462
DB 904 TGCTGGATCACAGGCTTTGGCAAGACCGAGGGAGACAGATGACAGACATCCCCCTTCCTC 963
QY 463 ArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyrLeuValTyrAsp 482
DB 964 CGGAGGTTGAGTCAATCTCATGCACTTCAAGAAATGCATGACTACTTGGTCTATGAC 1023
QY 483 SerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGlyArgAspSerCys 502
DB 1024 AGTTACCTTACCCCAAGGATGATGTGCTGGGGACCTTCGTGGGGGAGAGACTCCTGC 1083
QY 503 GlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArgTyrTrpLeuAlaGly 522
DB 1084 CAGGAGAGACAGCGGGGGGCTCTTGTCTGTGAGCAGAGACAAACCCGCTGGTACTTGCAG 1143
QY 523 ValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysProGlyValTyrThrLysVal 542
DB 1144 GTACACAGCTGGGGCACAGGCTGTGGCCAGAGAAACAAACCTGGGTGTGTACACCAAGTG 1203
QY 543 ThrGluValLeuProTrpIleTyrSerLysMetGluSerGluValArgPheArgLysSer 562
DB 1204 ACAGAGTTCTTCTCTGGATTATACAGCAGATGGAGAGCGAGGAGGAGTCCGATTCACAAATCC 1263
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US-09-879-792-12 (1-562) x US-09-879-792-35 (1-1230)

QY 180 LeuPheGlnPheTrpGlnGlyHisThrGlyIleArgTyrLysGluGlnArgGluSerCys 199
Db 28 CTAAGTCAGTTCTGGCGAGNNCCACACAGNNATCAGTACAGGAGCAGGAGAGCTGT 87
QY 200 ProLysHisAlaValArgCysAspGlyValValAspCysLysLeuLysSerAspGluLeu 219
Db 88 CCCAAGCAGCTGTTCCGTGTGACGGGGTGGTGGACTGCAAGCTGAAGAGTACGAGCTG 147
QY 220 GlyCysValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGlySerSerHis 239
Db 148 GGCCTGGTGAAGTTGACTGGGACCAAGTCTCTGCTTTAAATCTACTCTGGGCTCCCTCCAT 207
QY 240 GlnTrpLeuProLysCysSerSerAnTrpAnAspSerTyrSerGluLysThrCysGln 259
Db 208 CAGTGGCTTCCCATCTGTAGAGCAACTGGATGACTCTCTATCAGAGAAGACTGCCAG 267
QY 260 GlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaAn 279
Db 268 CAGCTGGGTTTCCAGAGTCTCACCGGACACCGAGTTGCCACACAGGATTTTGGCAAC 327
QY 280 SerPheSerIleLeuArgTyrAnSerThrIleGlnGluSerLeuHisArgSerGluCys 299
Db 328 AGCTTCTCAATCTTGAGATACAACTCCACCATCCAGAAAGCTCCACAGGCTCTGAATGC 387
QY 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThrGly 319
Db 388 CCTTCCAGCGGTATATCTCTCCAGTGTTCCTCAGTCTGGGACTGAGGGCCATGACCGG 447
QY 320 ArgIleValGlyGlyAlaLeuAlaSerAspSerLysTyrProTrpGlnValSerLeuHis 339
Db 448 CGGATCGTGGAGGGCGCTGGCTCGCATAGCAAGTGGCCCTTGGCAAGTGTGCGAC 507
QY 340 PheGlyThrThrHisIleCysGlyGlyThrIleAspAlaGlnTrpValLeuThrAla 359
Db 508 TTCGGACCAACCACATCTGTGGAGCAGCTCATTTGACGCCAGTGGGTGTCTCATGCC 567
QY 360 AlaHisCysPhePheValThrArgGluLysValLeuGluGlyTrpLysValTyrAlaGly 379
Db 568 GCCCACTGCTTCTGTGACCGGAGAGGTCCTGGAGGCTGAGAGTGTACGGGCG 627
QY 380 ThrSerAnLeuHisGlnLeuProGluAlaSerIleAlaGluIleIleLeuSer 399
Db 628 ACCAGCAACCTGCACAGTTGCTCAGGAGCGCTCCATTTGCCAGATCATCATCAACAGC 687
QY 400 AnTrpThrAspGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysProLeu 419
Db 688 AATACACGATGAGAGAGCACTATGACATCGCCCTCATCGGGCTGTCCAAGCCCTG 747
QY 420 ThrLeuSerAlaHis-----IleHisProAlaCysLeuProMetHisGly 434
Db 748 ACCCTGTCCGGTGGAGGAATCTGCACCTCCCGCTCTCTGCTGCCCGCCAGCACCT 807
QY 435 ---GlnThrPheSerLeuAnGluThrCysTrpIleThrGlyPheGlyLysThrArgGlu 453
Db 808 CTGCAGCCCTCGCATCTGTGCAGCATCT-----GTCAACTCATATCCGGGCCCCCAAGCT 861
QY 454 ThrAspAspLysThrSerPheLeuArgGluValGlnValAnLeuLeuAspPheLys 473
Db 862 TCTGCAGACACACATCCCTTCTCCGGAGGTGCGAGTCAATCTCATCGACTTCAAG 921
QY 474 LysCysAnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGly 493
Db 922 AAATGCAATGACTACTTGTCTATGACAGTTACCTTACCCCAAGCATGATGTGTCTGG 981
QY 494 AspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGlu 513
Db 982 GACCTTCGTGGGGCAGAGACTCCCTGGCCAGGAGACAGCGGGGGCCCTCTTGTCTGAG 1041
QY 514 GlnAnAnArgTyrTrpLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArg 533

Db 1042 CAGAAACAACCGCTGGTACTGCTGGCAGGTGTACACAGCTGGGGCACAGGCTGTGGCCACAGAGA 1101
QY 534 AnLysProGlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMet 553
Db 1102 AACAAACCTGGTGTGTACACCAAGTGCAGAAAGTTCTTCCCTGGATTTACAGCAAGATG 1161
QY 554 GluSerGluValArgPheArgLysSer 562
Db 1162 GAGGC-GAGGTGCGATTGAGAAATCC 1187

RESULT 10

US-09-804-156-5
; Sequence 5, Application US/09804156
; Patent No. US20020068320A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P4
; CURRENT APPLICATION NUMBER: US/09/804,156
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,025
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-156-5

Alignment Scores:
Pred. No.: 1,75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: Gaps: 0

US-09-879-792-12 (1-562) x US-09-804-156-5 (1-1222)

QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
Db 10 CACAGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTCGGACTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrp 334
Db 70 AGGGCATGACCGGGCGGATGTGGAGGGGGCTGGGCTCGAGTAGCAAGTGGCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGln 354
Db 130 CAAAGTGAGTCTGCACTTCGGCACCCACCATCTGTGGAGGCACTCATTCAGCCCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTrp 374
Db 190 TGGGTGCTCATCTGGCGCCACTGCTTCTTGTGACCCCGGAGAGGTCTCTGAGGGGCTGG 249
QY 375 LysValTyrAlaGlyThrSerAnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
Db 250 AAGGTGTACGGCGGACCGGACACTGTCACCACTGTTGCTTGAGCGAGCTTCAATCCCGAG 309
QY 395 IleIleIleAnSerAnTrpThrAspGluAspAspTyrAspIleAlaLeuMetArg 414
Db 310 ATCATCATCAACAGCAATTTACACCGATGAGGAGACGACTATGACATCGCCCTCATGCGG 369
QY 415 LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
Db 370 CTGTCCAAAGCCCTTGACCCCTGTCCGCTCACATCCACCTGCTGCTCCCATGTCATGGA 429
QY 435 GlnThrPheSerLeuAnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
Db 430 CAGACCTTACCTCAATGAGACCTGCTGGATCACAGCTTTGGCAGACAGCAGGAGACA 489
QY 455 AspAspLysThrSerProPheLeuArgGluValGlnValAnLeuIleAspPheLysLys 474

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Db      490  GATGACAGACATCCCTTCTCCGGAGGTCAGGTCAATCTCATCGACTTCAAGAAA 549
QY      475  CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
Db      550  TGCATAGTACTTGTGTCTATGACAGTTACCTTACCCCAAGCATGATGTGTCTGGGAC 609
QY      495  LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGln 514
Db      610  CTTCTGTGGGGGAGAGACTCTCTGCCAGGGAGACAGCGGGGGGCTCTCTGTCTGTGAGCAG 669
QY      515  AsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsn 534
Db      670  AACACCGCTGTACTCTGCAGGTTCACAGCTGGGGCAGAGGCTGTGGCCAGAGAAAC 729
QY      535  LysProGlyValTyrThrLysValThrGluValLeuProTyrPileTyrSerLysMetGlu 554
Db      730  AAACCTGGTGTGTACACCAAGTGCAGAGTTCCTCCCTGGATTTACAGCAAGATGGAG 789
QY      555  SerGluValArg 558
Db      790  AACAGAGCTCAG 801

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RESULT 11

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US-09-946-633-3
; Sequence 3, Application US/09946633
; Patent No. US20020119925A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/09/946,633
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-633-3

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Alignment Scores:

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Pred. No.: 1,75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 10 Gaps: 0

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US-09-879-792-12 (1-562) x US-09-946-633-3 (1-1222)

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QY      295  HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
Db      10  CACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTG 69
QY      315  ArgAlaMetThrGlyArgIleValGlyGlyAlaLeuAlaSerAspSerLysTyrProTyr 334
Db      70  AGGGCCATGACCGGGCGGATCGTGGAGGGGCGCTGGCTCGGATAGCAAGTGGCTTGG 129
QY      335  GlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGln 354

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Db      130  CAAAGTGAGTCTGCATCTTCGGGCACCCACCATCTCTGTGGAGGCACCGCTCATTTGACGCCAG 189
QY      355  TrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyr 374
Db      190  TGGGTGCTCACTGCCGCCACCTGCTTCTTGTGTGACCCGGGAGAGAGGTCTCTGGAGGGCTGG 249
QY      375  LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
Db      250  AAGGTGTATACCGGGACCCAGCAACCTGCACACCTGCTGCTGCTGAGCGACGCTCCATTGCCAG 309
QY      395  IleIleIleAsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
Db      310  ATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCCGCCCTCATGCCG 369
QY      415  LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
Db      370  CTGTCCAGGCCCTGACCTGCTCCGCTCATCATCCACCTGCTTGTGCTTCCCTCCCATGCA 429
QY      435  GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
Db      430  CAGACCTTTAGCCTCAATGAGACCTGCTGATCAGAGGCTTTGGCAAGACCCAGGGAGACA 489
QY      455  AspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLys 474
Db      490  GATGACAGACATCCCTTCTCCGGAGGTCAGGTCAATCTCATCTCATGCACTTCAAGAAA 549
QY      475  CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
Db      550  TGCATAGTACTTGTGTCTATGACAGTTACCTTACCCCAAGCATGATGTGTCTGGGAC 609
QY      495  LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGln 514
Db      610  CTTCTGTGGGGGAGAGACTCTCTGCCAGGGAGACAGCGGGGGGCTCTCTGTCTGTGAGCAG 669
QY      515  AsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsn 534
Db      670  AACACCGCTGTACTCTGCAGGTTCACAGCTGGGGCAGAGGCTGTGGCCAGAGAAAC 729
QY      535  LysProGlyValTyrThrLysValThrGluValLeuProTyrPileTyrSerLysMetGlu 554
Db      730  AAACCTGGTGTGTACACCAAGTGCAGAGTTCCTCCCTGGATTTACAGCAAGATGGAG 789
QY      555  SerGluValArg 558
Db      790  AACAGAGCTCAG 801

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RESULT 12

US-10-319-519-5

; Sequence 5, Application US/10319519

; Publication No. US20030175938A1

; GENERAL INFORMATION:

; APPLICANT: Shi et al.

; TITLE OF INVENTION: Serine Protease Polynucleotides, Polypeptides, and Antibodies

; FILE REFERENCE: PT005P5

; CURRENT APPLICATION NUMBER: US/10/319,519

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: US 10/125,459

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: US 09/597,842

; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: US 09/597,843

; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: US 10/067,761

; PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 09/946,633

; PRIOR FILING DATE: 2001-09-06

; PRIOR APPLICATION NUMBER: US 09/804,156

; PRIOR FILING DATE: 2001-03-13

; PRIOR APPLICATION NUMBER: US 09/597,839

; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: PCT/US00/12207

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: US 60/189,025

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; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/162,979
; PRIOR FILING DATE: 1999-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-319-519-5

Alignment Scores:
Pred. No.: 1,75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservatives: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 13 Gaps: 0

US-09-879-792-12 (1-562) x US-10-319-519-5 (1-1222)
QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
DB 10 CACAGGTCTGATGCGCTTCCAGCGGTATATCTCCCTCCAGTGTCCACTGCGGACTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTrp 334
DB 70 AGGGCCATGACCGGGCGGATCGTGGAGGGGGCTGGCTCGGATAGCAAGTGGCCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrHisIleCysGlyGlyThrIleuLeuAspAlaGln 354
DB 130 CAAGTGAGTCTGACTTGGCACCACCCACATCTGTGGAGGCGCCTCATTCAGCGCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPheValThrArgGluLysValLeuGluGlyTrp 374
DB 190 TGGGTGCTCAGTCCGCCCTCTTCGTGACCGGGAGAGGTCTCTGGAGGGCTGG 249
QY 375 LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
DB 250 AAGGTGTACGGGGGACCCAGCAACCTGCACCAAGTGTGCTGAGGCGCCTCCATTCGCGAG 309
QY 395 IleIleIleAsnSerAspTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
DB 310 ATCATCATCAACAGCAATTTACCCGATGAGGAGGACGACTATGATCGCCCTCATGGCG 369
QY 415 LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
DB 370 CTGTCCAAAGCCCTGACCTGTCGCTCACATCCACCTGCTTGCCTCCCATGTCATGGA 429
QY 435 GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
DB 430 CAGACCTTTAGCCTCAATGAGACCTGCTGGATCACAGGCTTTGGCAAGACCCAGGAGACA 489
QY 455 AspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuLeuAspPheLysLys 474
DB 490 GATGACACAGCAATTCCTCTCCGGAGGTCGAGGTCAATCTCATCGACTTTCAAGAAA 549
QY 475 CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
DB 550 TGCATATGACTACTTGTGTATGACAGTTACCTTACCCCAAGGATGATGTGTCTGGGAC 609
QY 495 LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGln 514
DB 610 CTTCTGGGGGGCAGAGACTCTCCGCCAGGGAGACAGCGGGGGGCTCTGTCTGTGAGCAG 669
QY 515 AsnAsnArgTyrTyrIleAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsn 534
DB 670 AACACCGCTGTGTA CTTGCGACGGTGTACCACTGGGGGCACAGGCTGTGGCCAGAGAAC 729
QY 535 LysProGlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGlu 554
DB 730 AAACCTGGTGTGTACACCAAAAGTGA CAGAAGTTCTTCCCTGGATTTTACAGCAAGATGGAG 789
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QY 555 SerGluValArg 558
DB 790 AACAGAGCTCAG 801

RESULT 13
US-10-125-459-3
; Sequence 3, Application US/10125459
; Publication NO. US20020192800A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-459-3

Alignment Scores:
Pred. No.: 1,75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservatives: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 14 Gaps: 0

US-09-879-792-12 (1-562) x US-10-125-459-3 (1-1222)
QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
DB 10 CACAGGTCTGATGCGCTTCCAGCGGTATATCTCCCTCCAGTGTCCACTGCGGACTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTrp 334
DB 70 AGGGCCATGACCGGGCGGATCGTGGAGGGGGCTGGCTCGGATAGCAAGTGGCCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrHisIleCysGlyGlyThrIleuLeuAspAlaGln 354
DB 130 CAAGTGAGTCTGACTTGGCACCACCCACATCTGTGGAGGCGCCTCATTCAGCGCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPheValThrArgGluLysValLeuGluGlyTrp 374
DB 190 TGGGTGCTCAGTCCGCCCTCTTCGTGACCGGGAGAGGTCTCTGGAGGGCTGG 249
QY 375 LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
DB 250 AAGGTGTACGGGGGACCCAGCAACCTGCACCAAGTGTGCTGAGGCGCCTCCATTCGCGAG 309
QY 395 IleIleIleAsnSerAspTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
DB 310 ATCATCATCAACAGCAATTTACCCGATGAGGAGGACGACTATGATCGCCCTCATGGCG 369
QY 415 LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
DB 370 CTGTCCAAAGCCCTGACCTGTCGCTCACATCCACCTGCTTGCCTCCCATGTCATGGA 429
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QY 435 GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
Db 430 CAGACCTTTAGCCTCAATGAGACCTGCTGGATCACAGGCTTTGGCAAGACCGAGGAGACA 489
QY 455 AspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLys 474
Db 490 GATGACAGACATCCCTTCTCCGGGAGGTGCAGGTCAATCTCATGACTTCAGAAA 549
QY 475 CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
Db 550 TGCAATGACTACTTGGTCTATGACAGTTACCTTACCCCAAGGATGATGTGCTGGGAC 609
QY 495 LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGln 514
Db 610 CTTCGTGGGGGAGAGACTCCCTGCGAGGAGACAGCGGGGGGCTCTTGTCTGTGAGCAG 669
QY 515 AsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsn 534
Db 670 AACACCGCTGGTACTGCGAGGTGTCCACAGCTGGGGCAGAGGTGTGGCCAGAGAAC 729
QY 535 LysProGlyValTyrThrLysValThrGluValLeuProTyrIleTyrSerLysMetGlu 554
Db 730 AAACCTGGTGTATACCAAAAGTGACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGAG 789
QY 555 SerGluValArg 558
Db 790 AACAGAGCTCAG 801

RESULT 14
US-10-067-761-5
; Sequence 5, Application US/10067761
; Publication No. US20020197701A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT00594
; CURRENT APPLICATION NUMBER: US/10/067,761
; PRIORITY FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 09/804,156
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,025
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-761-5

Alignment Scores:
Pred. No.: 1.75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 14 Gaps: 0

US-09-879-792-12 (1-562) x US-10-067-761-5 (1-1222)
QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
Db 10 CACAGGCTGATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCATCTGCGAGCTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTyrProTyr 334
Db 70 AGGGCCATGACCGGGCGGATCGTGGAGGGCGCTGGCTCGATAGCAAGTGGCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGln 354
Db 130 CAAGTGAGTCTGCACTTCGGCACCCACCATCTGTGGAGGACGCTCATTTAGCGCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTrp 374
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Db 190 TGGGTGCTCAGTCGCGCCACCTGCTTCTTGTGACCGCGAGAGGTCTCTGGAGGCTG 249
QY 375 LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
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QY 395 IleIleIleAsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
Db 310 ATCATCATCAACAGCAATTTACACCGATGAGGAGGAGCAGCTATGACATCGCCCTCATGCGG 369
QY 415 LeuSerLysProLeuThrIleuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
Db 370 CTGTCCAAAGCCCTGACCCCTGCTCCCTCACATCCACCTGCTTGCCTCCCATGCTGCA 429
QY 435 GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
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QY 495 LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGln 514
Db 610 CTTCGTGGGGGAGAGACTCCCTGCGAGGAGACAGCGGGGGGCTCTTGTCTGTGAGCAG 669
QY 515 AsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsn 534
Db 670 AACACCGCTGGTACTGCGAGGTGTCCACAGCTGGGGCAGAGGTGTGGCCAGAGAAC 729
QY 535 LysProGlyValTyrThrLysValThrGluValLeuProTyrIleTyrSerLysMetGlu 554
Db 730 AAACCTGGTGTATACCAAAAGTGACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGAG 789
QY 555 SerGluValArg 558
Db 790 AACAGAGCTCAG 801

RESULT 15
US-09-879-792-28
; Sequence 28, Application US/09879792
; Patent No. US20020061850A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; APPLICANT: Gedrich, Richard
; TITLE OF INVENTION: Regulation of Human Transmembrane Serine
; TITLE OF INVENTION: Protease
; FILE REFERENCE: 02973.00035
; CURRENT APPLICATION NUMBER: US/09/879,792
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/211,224
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/283,353
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,648
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-792-28

Alignment Scores:
Pred. No.: 2.65e-86 Length: 834
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(Docket No. US20020061850A1 LIO-81-WO)

Score: 1282.50 Matches: 266
Percent Similarity: 95.39% Conservative: 3
Best Local Similarity: 94.33% Mismatches: 10
Query Match: 42.76% Indels: 9
DB: 9 Gaps: 0

US-09-879-792-12 (1-562) x US-09-879-792-28 (1-834)

QY 219 LeuGlyCysValArgPheAspTyrAspLysSerLeuLeuLysIleTyrSerGlySerSer 238
Db 2 CTGGGCTGGTGAGGTTTGACTGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTCC 61

QY 239 HisGlnTyrLeuProIleCysSerSerAsnTyrAsnAspSerTyrSerGlyLysThrCys 258
Db 62 CATCAGTGGCTTCCCATCTGTAGCAGCAACTGGAAATGACTCTCTACTCAGAGAAGACCTGC 121

QY 259 GlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAla 278
Db 122 CAGCAGCTGGGTTTGGAGGTGCTCACCGGACAAACGAGGTGGCCACAGGGATTTTGCC 181

QY 279 AsnSerPheSerIleLeuArgTyrAsnSerThrIleGlnGluSerLeuHisArgSerGlu 298
Db 182 AACAGCTTCTCAATCTGAGATACAACTCCACCATCCAGAAAGCTCCACAGGTCTGAA 241

QY 299 CysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThr 318
Db 242 TGCCCTTCCACGGGTATATCTCCCTCCAGTGTCCCACTGCGGACTGAGGGCCATGACC 301

QY 319 GlyArgIleValGlyAlaLeuAlaSerAspSerLysTyrProTyrGlnValSerLeu 338
Db 302 GGGCGGATCGTGGAGGGGCGTGGCTCGGATAGCAAGTGGCTTGGCAAGTGGTCTG 361

QY 339 HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTyrValLeuThr 358
Db 362 CACTTCGGCACCCACCATCTGTGGAGGACGCTCATTTGACGCCCGCAGTGGGTGCTCACT 421

QY 359 AlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAla 378
Db 422 GCGGCCCATCTGCTTCTGTGACCCGGAGAGGTCTTGAGGGGCTGGAGGTGTACGGC 481

QY 379 GlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleLeu 398
Db 482 GGCACCAAGCACTG-CACCAGTTGCTTGAGGCAGC-TCCATTGCCGAGATCATCATCAAC 539

QY 399 SerAsnTyrThrAspGluGluAspAspTyr-AspIleAlaLeuMetArgLeu-SerLysP 418
Db 540 AGCAATTACCGGATGAGGAGGACGACTATTGACATCGCCCTCATGCGGCTGTCCAAGC 599

QY 418 roLeuThrLeuSerAlaHisIleHisProAlaCysLeu-ProMetHisGlyGlnThrPhe 437
Db 600 CCTGAACCTGTCCGT-CACATCCACCCTTGCTTGCTCCCATGATGGACAGACCTTT 658

QY 438 SerLeuAsnGluThrCysTyrIleThrGlyPheGlyLysThrArgGluThrAspAspLys 457
Db 659 AGCCTCAATGAGACCTGTGGATCACAGGCTTTGGCAAGACAGAGGAGACAGATCAAAAG 718

QY 458 ThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAsp 477
Db 719 ACATCCCCCTTCCCT-CGGAGGTGAGGTCAATCTCATGCACTTCCAGAAATGCAATGAC 777

QY 478 TyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGly 497
Db 778 TAACTGGTCTATGACAGTACCTTAC--CCAGGATGATGTGTGT-GGGGAACCTCTGTGG 834

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Job time : 484 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 17, 2003, 20:10:37 ; Search time 104 Seconds

(without alignments)
2385.167 Million cell updates/sec

Title: US-09-879-792-12

Perfect score: 2999

Sequence: 1 MERDSHGNSPARTPSAGAS.....TEVLPWYKMESEVRFKKS 562

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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6: /cgm2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	736.5	24.6	2479	3	US-09-342-749-29
4	736.5	24.6	2479	4	US-09-691-840-29
5	727.5	24.3	2413	3	US-09-518-046-1
6	713	23.8	2079	4	US-09-656-002-1
7	707.5	23.6	2544	3	US-09-518-046-3
8	707.5	23.6	2038	3	US-09-008-271A-18
9	694.5	23.2	2416	3	US-09-261-416-1
10	666	22.2	2363	4	US-09-742-703-3
11	642.5	21.4	1783	3	US-09-510-738A-188
12	642.5	21.4	1783	4	US-09-861-966-188

13	622.5	20.8	610	4	US-09-280-116-22	Sequence 22, Appl
14	619.5	20.7	1605	2	US-09-000-846-1	Sequence 1, Appl
15	612	20.4	1615	2	US-09-820-002-1	Sequence 1, Appl
16	594.5	19.8	1077	3	US-08-807-151-2	Sequence 2, Appl
17	594.5	19.8	1077	4	US-09-478-957-2	Sequence 2, Appl
18	584.5	19.5	3147	2	US-09-027-337-1	Sequence 1, Appl
19	584.5	19.5	3147	4	US-09-644-600-1	Sequence 1, Appl
20	584.5	19.5	3147	4	US-09-644-600-18	Sequence 18, Appl
21	548.5	18.3	2581	5	PCT-US94-00616-1	Sequence 1, Appl
22	548.5	18.3	2581	5	PCT-US94-00616-1	Sequence 1, Appl
23	524.5	17.5	2900	2	US-09-027-337-9	Sequence 9, Appl
24	524.5	17.5	2900	2	US-09-027-337-9	Sequence 9, Appl
25	520	17.3	1724	6	5200340-5	Patent No. 5200340
26	513.5	17.1	11081	3	US-09-008-271A-15	Sequence 15, Appl
27	512	17.1	11081	3	US-09-016-366A-24	Sequence 24, Appl
28	510.5	17.0	11094	4	US-09-023-942A-3	Sequence 3, Appl
29	508.5	17.0	11094	4	US-09-023-942A-5	Sequence 5, Appl
30	508	16.9	1097	2	US-08-978-404B-4	Sequence 4, Appl
31	505	16.8	1108	2	US-09-016-366A-14	Sequence 14, Appl
32	505	16.8	1108	2	US-08-978-404B-20	Sequence 20, Appl
33	502	16.7	1739	2	US-08-681-151-2	Sequence 2, Appl
34	501	16.7	959	4	US-09-023-942A-25	Sequence 25, Appl
35	500	16.7	1142	4	US-09-386-642-8	Sequence 8, Appl
36	500	16.7	1169	4	US-09-386-642-7	Sequence 7, Appl
37	493.5	16.5	2296	1	US-07-750-080A-18	Sequence 18, Appl
38	493.5	16.5	2296	3	US-08-651-472-18	Sequence 18, Appl
39	493.5	16.5	2296	3	US-08-358-928-18	Sequence 18, Appl
40	493.5	16.5	2430	4	US-09-192-012-4	Sequence 4, Appl
41	493.5	16.5	2679	6	5200340-7	Patent No. 5200340
42	493.5	16.5	2753	1	US-07-854-603-1	Sequence 1, Appl
43	492.5	16.4	2497	1	US-08-643-219-12	Sequence 12, Appl
44	492.5	16.4	2497	2	US-09-131-995-12	Sequence 12, Appl
45	492.5	16.4	2497	2	US-08-832-087B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-342-749-1
; Sequence 1, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TWERS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329


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FEATURE:
NAME/KEY: conflict
LOCATION: (1466)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
FEATURE:
NAME/KEY: conflict
LOCATION: (1471)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
FEATURE:
NAME/KEY: allele
LOCATION: (478)
OTHER INFORMATION: This base can be G or A with G being the more
OTHER INFORMATION: common allele. The codon will change from Val to
OTHER INFORMATION: Met.
FEATURE:
NAME/KEY: allele
LOCATION: (777)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. The codon is unaffected with both
OTHER INFORMATION: alleles encoding Gly.
FEATURE:
NAME/KEY: allele
LOCATION: (768)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. This is a silent polymorphism.
FEATURE:
NAME/KEY: allele
LOCATION: (834)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. This is a silent polymorphism.
FEATURE:
NAME/KEY: allele
LOCATION: (625)
OTHER INFORMATION: This base can be T or A with T being the more
OTHER INFORMATION: common allele. The codon will change from Phe to
OTHER INFORMATION: Ile
US-09-342-749-1

Alignment Scores:
Pred. No.: 2,716-30 Length: 1479
Score: 740.50 Matches: 178
Percent Similarity: 47.49% Conservative: 87
Best Local Similarity: 31.90% Mismatches: 194
Query Match: 24.69% Indels: 99
Db: 3 Gaps: 18

US-09-879-792-12 (1-562) x US-09-342-749-1 (1-1479)

QY 27 AlaGlyThrProGlyArgAla-----SerProAlaGln 38
Db 13 TCAGGTCACCCAGCCTATTGGACCTTACTATGAAACCATGGATACCAACCGGAAAC 72
QY 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGln 58
Db 73 CCTATCCGCGCAGCCCACTGTGTCCTCCACT---GTCTACGAGTGTGATCGGCTCAG 129
QY 59 AlaSerProAlaGlyThrProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
Db 130 TACTACCGTCCTCCCGTCGCC-----CAGTACGCCCGGAGGTC 168
QY 79 AlaSerProAlaArgAlaSerProAlaLeuAlaSerLeuSerArgSerSerGlyArg 98
Db 169 CTGACGCGGCT---TCCAACCCCGTCGTGTCAGCAGCCCAATCCCATCCCGG--- 222
QY 99 SerSerAlaArgSerAlaSerValThrThrSerProThrArgValThrLeuValArg 118
Db 223 -----ACAGTGTGCACCTCAAGACTTAAGAACCTGTGCTC 261
QY 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
Db 262 ACCTTGACCTGGGACCTTC----- 282
QY 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTyrArgGluGlyGln 158

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Db 282 ----- 282
QY 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuLeuLeuValValSerLeuLeu 178
Db 283 -----CTCGTGGAGCT-----GCGTGGCGCTGCGCTACTC 315
QY 179 IleLeuPheGlnPheTyrGln-----GlyHisThrGlyLeuArgTyr 192
Db 316 -----TGGAGTTCATGGGAGCGACAGTCTCCAACTCTGGGATAGAGTGC 360
QY 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValAlaAspCys 212
Db 361 ---GACTCTCTCAGGTACCTGATCAACCCCTCTAAGTGTGTGATGGGTGCACACTGC 417
QY 213 LysLeuLysSerAspGlnLeuGlyCysValArgPheAspTyrPaspLysSerLeuLeuLys 232
Db 418 CCGCGCGGAGGAGCAGAAATCGGTGTGTTCGCTCTACGGACCAAACTTCATCTTCAG 477
QY 233 IleTyrSerGlySerSerHisGlnTyrLeuProIleCysSerSerAsnTyrAsnAspSer 252
Db 478 GTGTACTCATCTCAGAGGAGTCTGACCCCTGTGTGCCAAGACGACTGGACGAGAAC 537
QY 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrGluVal 272
Db 538 TACGGCGCGGCGCTGCGAGGACATGGCTATAGATAATATTTTACTCTAGCCAA--- 594
QY 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db 595 GGAATAGTGGATGACAGCGGATCCACAGCTTTATGAAACTGAACACAAAGTGGCGCAAT 654
QY 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306
Db 655 GTGATATCTATATAAACTGTACCAAGTGTGCTGTCTTCAAAGCAGTGGTTCCT 714
QY 307 LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db 715 TTACGCTGTATAGCTTGGCGGTCAACTTGAACCTCAAGCGCGCAGAGGAGTGTGGGC 774
QY 324 GlyAlaLeuAlaSerAspSerLysTyrProTyrGlnValSerLeuHisPheGlyThrThr 343
Db 775 GCGGAGAGCGCGCTCCCGGGGCGCTGCGCTGCGAGTGCAGCTGCACGTCAGAACGTC 834
QY 344 HisIleCysGlyGlyThrLeuIleAspAlaGlnTyrValLeuThrAlaAlaHisCysPhe 363
Db 835 CAGTGTGCGGAGGCTCCATCATCACCCCGAGTGTGTGACAGCCGCCACTCGCTG 894
QY 364 PheValThrArgGluLysValLeuGluGly-----TyrLysValTyrAlaGlyThr 380
Db 895 -----GAAAAACCTCTTAACAATCCATGGCATTTGACGCGCATTTGGCGGATT 942
QY 381 SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db 943 TTGAGACAATCTTTCTATGTTCTATGAGCCCGGATACCAAGTAGAATAAGTATTTCTCAT 1002
QY 399 SerAsnTyrThrAspGluGluAspTyrAspIleAlaLeuMetArgLeuSerLysPro 418
Db 1003 CCAATATGACTCCAGACCAAGACATGACATGCTGCTGATGAGCTGCAGAGCTC 1062
QY 419 LeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db 1063 CTGACTTTCAACGACCTAGTGAACCACTGTGTCTGCCCAACCCAGGATGATGTGTCAG 1122
QY 439 LeuAlaGlnThrCysTyrIleThrGlyPheGlyThrArgGluThrAspAspLysThr 458
Db 1123 CCAGAACAGCTCTGCTGATTTCCGGGTGGGGGCCACCCAGAGAG---AAAGGGAGAGCC 1179
QY 459 SerProPheLeuArgGluValGlnValAsnLeuLeuAspPheLeuLysCysAsnAspTyr 478
Db 1180 TCAGAGTGTGAGCGCTGCCAGGTGCTTCTCATTTGAGACACAGAGATGCAACAGCAGA 1239
QY 479 LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGly 498

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Db 1240 TATGCTATGACAACTGATCACACCGCCGATGATGTCGGCGCTTCTCGCAGGGGAAAC 1299
 Qy 499 ArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGlnGlnAsnAsnArgTTP 518
 Db 1300 GTCGATTCTTCCAGGGTGACAGTGGAGGGCTCTGTCTCACTTCCGAAGAACAAATATCTGG 1359
 Qy 519 TyrIleuAlaGlyValThrSerTTPGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
 Db 1360 TGGCTGATAGGGGATACAAGCTGGGGTTCTGGCTGTGCCAAAGCTTACAGCAGGAGTG 1419
 Qy 539 TyrThrLysValThrGluValLeuProTTPLeuTyrSerLysMetGluSerGlu 556
 Db 1420 TACGGGAATGTGATTCACGAGCTGGATTATCGACAAATGAGGGCAGAC 1473

RESULT 2

US-09-691-840-1
 ; Sequence 1, Application US/09691840
 ; Patent No. 6444419
 ; GENERAL INFORMATION:
 ; APPLICANT: Wong, Alexander K.C.
 ; APPLICANT: Tavtigian, Sean V.
 ; APPLICANT: Teng, David H.-F.
 ; APPLICANT: Myriad Genetics, Inc.
 ; TITLE OF INVENTION: TWPRSS2 is a Tumor Suppressor
 ; FILE REFERENCE: 2318-202
 ; CURRENT APPLICATION NUMBER: US/09/691,840
 ; CURRENT FILING DATE: 2000-10-18
 ; PRIOR APPLICATION NUMBER: US/09/342,749
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: US 60/091,044
 ; PRIOR FILING DATE: 1998-06-29
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 1479
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1476)
 ; NAME/KEY: conflict
 ; LOCATION: (724)
 ; OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
 ; NAME/KEY: conflict
 ; LOCATION: (985)
 ; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
 ; NAME/KEY: conflict
 ; LOCATION: (1347)
 ; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
 ; NAME/KEY: conflict
 ; LOCATION: (1466)
 ; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
 ; NAME/KEY: conflict
 ; LOCATION: (1471)
 ; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
 ; NAME/KEY: allele
 ; LOCATION: (478)
 ; OTHER INFORMATION: This base can be G or A with G being the more
 ; OTHER INFORMATION: common allele. The codon will change from Val to
 ; OTHER INFORMATION: Met.
 ; NAME/KEY: allele
 ; LOCATION: (777)
 ; OTHER INFORMATION: This base can be C or T with C being the more
 ; OTHER INFORMATION: common allele. The codon is unaffected with both
 ; OTHER INFORMATION: alleles encoding Gly.
 ; NAME/KEY: allele
 ; LOCATION: (768)
 ; OTHER INFORMATION: This base can be C or T with C being the more
 ; OTHER INFORMATION: common allele. This is a silent polymorphism.
 ; NAME/KEY: allele
 ; LOCATION: (834)
 ; OTHER INFORMATION: This base can be C or T with C being the more
 ; OTHER INFORMATION: common allele. This is a silent polymorphism.

; NAME/KEY: allele
 ; LOCATION: (625)
 ; OTHER INFORMATION: This base can be T or A with T being the more
 ; OTHER INFORMATION: common allele. The codon will change from Phe to Ile
 US-09-691-840-1
 Alignment Scores:
 Pred. No.: 2,71e-30 Length: 1479
 Score: 740.50 Matches: 178
 Percent Similarity: 47.49% Conservative: 87
 Best Local Similarity: 31.90% Mismatches: 194
 Query Match: 24.69% Indels: 99
 DB: 4 Gaps: 18
 US-09-879-792-12 (1-562) x US-09-691-840-1 (1-1479)
 Qy 27 AlaGlyThrProGlyArgAla-----SerProAlaGln 38
 Db 13 TCAGGGTCACCAACGCTATTGGACCTTACTATGAAACCATGATACCAACCGGAAAC 72
 Qy 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGln 58
 Db 73 CCTATCCGCGACAGCCCACTGTGTCCTCCACT--GTCTACGAGGTGCATCCGGCTCAG 129
 Qy 59 AlaSerProAlaGlyThrProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
 Db 130 TACTACCCGTCCTCCCGTGTCCCTC-----CAGTACGCCCCGAGGGTC 168
 Qy 79 AlaSerProAlaGlyThrProAlaLeuAlaSerProAlaLeuAlaSerSerSerGlyArg 98
 Db 169 CTGACGAGGCT---TCACCCCGTGTCTGACGAGGCCCAATCCCATCCGG--- 222
 Qy 99 SerSerSerAlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArg 118
 Db 223 -----ACAGTGTGCACCTCAAGACTAAGAAAGCACTGTGCATC 261
 Qy 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
 Db 262 ACCTTGACCTTGGGGACCTTC----- 282
 Qy 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTTPArgGluGln 158
 Db 282 ----- 282
 Qy 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValValSerLeuIle 178
 Db 283 -----CTCGTGGGAGCT-----GGCTGGCGCTGGCTACTC 315
 Qy 179 IleLeuPheGlnPheTTPGln-----GlyHisThrGlyIleArgTyr 192
 Db 316 -----TGAAGTTTCATGGCGCAGCAAGTCTCCAACTCTGGGATAGAGTGC 360
 Qy 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCys 212
 Db 361 ---GACTCTCTCAGTACTGTCATCAACCCCTCTAACTGTGTGTGATGGGTGTCACTGC 417
 Qy 213 LysLeuLysSerAspGluLeuGlyCysValArgPheAspTTPAspLysSerLeuLeuLys 232
 Db 418 CCGCGCGGGGAGGACGAGAAATCGGTGTGTTCCTCTACGCGACCAAACTTCATCTTCAG 477
 Qy 233 IleTyrSerGlySerSerHisGlnTTPLeuProIleCysSerSerAsnTTPAsnAspSer 252
 Db 478 GTGTACTCATCTCAGAGGAAAGTCTCTGGCACCTGTGTGCCAAGCACTGCAAGCAGAAC 537
 Qy 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluVal 272
 Db 538 TACGGCGGGGGCGCTCGAGGACATGGCTATGAAGATAATTTTACTCTAGCCAA--- 594
 Qy 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
 Db 595 GGAATAGTGGATGACAGCGGATCCACGAGCTTTATGAACCTGAACACAGTCCGCGCAAT 654
 Qy 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306

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Db 655 GTCCGATCTATATAAAAGCTACACAGTGTGCTCTTCAAAAAGCAGTGGTTCT 714
Qy 307 LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db 715 TTACGCTGTATAGCTCGGGGTCACTTGAACTCAAGCCGCCAGCAGGATCGTGGGC 774
Qy 324 GlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHisPheGlyThrThr 343
Db 775 GCGCAGAGCGCGCTCCCGGGGCGCTGGCCCTGGCAGGTCAGCCTGCAGCTCCAGAACGTC 834
Qy 344 HisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThrAlaAlaHisCysPhe 363
Db 835 CACGTGTGCGAGGCTCCATCATCACCCCGAGTGTATCGTGCACAGCGCCGCTCGGTG 894
Qy 364 PheValThrArgGlyLeuValLeuGly-----TrpLysValTyrAlaGlyThr 380
Db 895 -----GAANAACCTTTAAACATCCATGCCATTTGAGCGCATTTGCGGGATT 942
Qy 381 SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db 943 TTGAGACAACTTTTCATCTTCTATGAGCGCGATACCAAGTAGAAAGATGATTCTCAT 1002
Qy 399 SerAsnTyrThrAspGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysPro 418
Db 1003 CCAATTATGACTCCAGAGCAAGAACAAATGACATTTGCGCTGTGATGAAGCTCGAGAGCCT 1062
Qy 419 LeuThrLeuSerAlaHisIleProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db 1063 CTGACTTTCAACGACCTAGTGAACCAAGTGTCTGCCCAACCCAGGATGATGCTGCAG 1122
Qy 439 LeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspLysThr 458
Db 1123 CCAGAACACTCTGTGTGATTTCCGGTGGGGGCGCCACCGAGAG-----AAAGGGAAGACC 1179
Qy 459 SerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyr 478
Db 1180 TCAGAGTGTGAACGCTGCCAAGGTGTTCTCATTTGAGACACAGAGATGCAACAGCAGA 1239
Qy 479 LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGly 498
Db 1240 TATGCTATGACAACCTGATCACACAGCCATGATCTGTGCGGCTTCTTCGAGGGGAC 1299
Qy 499 ArgAspSerCysGlnGlyAspSerGlyCysProLeuValCysGluGlnAsnAsnArgTrp 518
Db 1300 GTCGATTTCTCCAGGGTGACAGTGGAGGGCTCTGTGCTCACTTCGAGAACAAATATCTGG 1359
Qy 519 TyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db 1360 TGGCTGATAGGGGATACAGCTGGGTTCTGGCTGTGCCAAGCTTACAGACCCAGAGTG 1419
Qy 539 TyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSerGlu 556
Db 1420 TACGGGAATGTGTGTTATTACGAGCTGGATTTATCGACAAATGAGGGCAGAC 1473
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RESULT 3

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US-09-342-749-29
; Sequence 29, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRPS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-749-29

Alignment Scores:
Pred. NO.: 7,75e-30 Length: 2479
Score: 736.50 Matches: 178
Percent Similarity: 47.40% Conservative: 86
Best Local Similarity: 31.96% Mismatches: 194
Query Match: 24.56% Indels: 99
DB: 3 Gaps: 18

US-09-879-792-12 (1-562) x US-09-342-749-29 (1-2479)

Qy 27 AlaGlyThrProProGlyArgAla-----SerProAlaGln 38
Db 69 TCAGGGTCACCCACCGACTATTGGACCTTACTATGAAACCATGGATACCAACCGAAAAAC 128
Qy 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProProGlyArgAlaSerProAlaGln 58
Db 129 CCCTATCCCGCACAGCCACTGTGTCCTCCACT---GTCTACGAGGTGCTATCCGGCTCAG 185
Qy 59 AlaSerProAlaGlyThrProProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
Db 186 TACTATCCCGTCCCGCGTCCCG-----CAGTACGCGCCCGAGGGTC 224
Qy 79 AlaSerProAlaArgAlaSerProAlaLeuAlaSerLeuSerArgSerSerSerGlyArg 98
Db 225 CTGACGAGGCT---TCAACCCCGTGTCTGCGACGAGCCCAATCCCATCCGG--- 278
Qy 99 SerSerSerAlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArg 118
Db 279 -----ACAGTGTGCACCTCAAGACTAAGAAAGCACTGTGCATC 317
Qy 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
Db 318 ACCTTGACCTCGGGGACCTTC----- 338
Qy 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArgGluGlyGln 158
Db 338 ----- 338
Qy 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValValSerLeuIle 178
Db 339 -----CTCGTGGGAGCT-----GGCTGGCGCTGGCTACTC 371
Qy 179 IleLeuPheGlnPheTrpGln-----GlyHisThrGlyIleArgTyr 192
Db 372 -----TGAAGTTTCATGGGCGAGCAAGTGTCTCAACTCTGGGATAGAGTGC 416
Qy 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCys 212
Db 417 ---GACTCTCTCAGGTACTGTGATCAACCCCTCTAACTGGTGTGTGATGGGTGTACACTGC 473
Qy 213 LysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeuLeuLys 232
Db 474 CCGCGCGGGAGGACGAGAAATCGGTGTGTTCCTCTACGAGCAACAACTTCATCTTCAG 533
Qy 233 IleTyrSerGlySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsnAspSer 252
Db 534 ATGTACTCATCTCAGAGGAAGTCTCTGGACCTGTGTGCCAAGACGACTGGAACGAGAAC 593
Qy 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluVal 272
Db 594 TACGGGGGGGGCGGCTCGAGGACATGGCTATAGAATAATTTTACTCTAGCCAA--- 650
Qy 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db 651 GGAATAGTGGATGACAGCGGATCCACCGACTTTATGAACTGTAACACACAGTGGCGGCAAT 710
Qy 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306
Db 306 ----- 306
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Db 711 GTCGATATCTATAAAAGCTGACACAGTGTGCTGTTCTTCAAAAGCAGTGGTTCT 770
Qy 307 LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db 771 TTACCTGTTAGCCTGCGGGCTCAACTTGAACCTCAAGCGCCAGACGAGATCGTGGGC 830
Qy 324 GlyAlaLeuAlaSerAspSerIleValProTTPGlnValSerLeuHisPheGlyThr 343
Db 831 GGTGAGAGCGGCTCCCGGGGCGCTGCGCCCTGGCAGGTGAGCTGCAGTCCAGAACGTC 890
Qy 344 HisIleCysGlyGlyThrLeuIleAspAlaGlnTTPValLeuThrAlaAlaHisCysPhe 363
Db 891 CACGTGCGGAGGCTCCATCATCACCCCGAGTGGATGTCGACAGCGCCCTCGCTGG 950
Qy 364 PheValThrArgGluIleValLeuGluGly-----TTPlysValTyrAlaGlyThr 380
Db 951 -----GAAAAACCTCTTAACATCCATGCGCATTCGACGCGCATTCGGGGATT 998
Qy 381 SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db 999 TTGACACATCTTCTGTTCTATGGAGCGGATACCAAGTACAAAAGTGAATTTCTCAT 1058
Qy 399 SerAsnTyrThrAspGluAspTyrAspIleAlaLeuMetArgLeuSerIleValPro 418
Db 1059 CCAAAATTATGACTCCAGACCAAGAACAAATGACATTCGCTGATGAAGCTGCAGAGCT 1118
Qy 419 LeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db 1119 CTGACTTTCACAGACCTAGTGAACAGTGTGTCTGCCCAACCCAGGCGATGATGTCGAG 1178
Qy 439 LeuAsnGluThrCysTyrIleThrGlyPheGlyLysThrArgGluThrAspAspIleThr 458
Db 1179 CCAGAACAGCTCTGCTGATTTCCGGGTGGGGGGCCACCGAGAG-----AAAGGGAAGACC 1235
Qy 459 SerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysCysAsnAspTyr 478
Db 1236 TCAGAAGTGTGAACGCTGCCAAGTGTCTTCTCATTTGACACACAGATGCAACAGCAGA 1295
Qy 479 LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGly 498
Db 1296 TATGCTATGACAACTGATACACACAGCCATGATCTGTGCGGCTTCTGCGGGGAAC 1355
Qy 499 ArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArgTTP 518
Db 1356 GTCGATTTCTGACAGGGTGACAGTGGAGGGCTCTGGTCACTTCGAAACACAAATATCTGG 1415
Qy 519 TyrLeuAlaGlyValThrSerTTPGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db 1416 TGGCTGATAGGGGATACAAAGTGGGGTCTGGCTGTGCCMAAGCTTACAGACCAGAGTG 1475
Qy 539 TyrThrLysValThrGluValLeuProTTPIleTyrSerLysMetGluSer 555
Db 1476 TACGGGAATGTGATGGTATTACGGACTGGATTTTATCGACAAATGAAGGCA 1526
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RESULT 4

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US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: THPRS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-840-29
```

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Alignment Scores:
Pred. No.: 7,75e-30 Length: 2479
Score: 736.50 Matches: 178
Percent Similarity: 47.40% Conservative: 86
Best Local Similarity: 31.96% Mismatches: 194
Query Match: 24.56% Indels: 99
DB: 4 Gaps: 18
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US-09-879-792-12 (1-562) x US-09-691-840-29 (1-2479)

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Qy 27 AlaGlyThrProGlyArgAla-----SerProAlaGln 38
Db 69 TCAGGTGTACACACAGCTATTGGACCTTACTATGAAAAACCATGGATACCAACCGGAAC 128
Qy 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGln 58
Db 129 CCTATCCCGCACAGCCCACTGTGTGCCACT---GTCACGAGGTGATCGGCTCAG 185
Qy 59 AlaSerProAlaGlyThrProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
Db 186 TACTACCGGTCCCGCGTGCCT-----CAGTACGCCCGGAGGTC 224
Qy 79 AlaSerProAlaArgAlaSerProAlaLeuAlaSerLeuSerSerSerSerGlyArg 98
Db 225 CTGACGCGAGCT---TCCAAACCCCTGCTGTCACGAGCCCAAAATCCCATCCGCG--- 278
Qy 99 SerSerSerAlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArg 118
Db 279 -----ACATGTGCACCTCAAGACTAAGAACACTGTGCATC 317
Qy 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
Db 318 ACCTTGACCTCGGGGACCTTC----- 338
Qy 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTyrArgGluGlyGln 158
Db 338 ----- 338
Qy 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValSerLeuIle 178
Db 339 -----CTCGTGGAGCT-----GCGCTGGCGCTCGCTACTC 371
Qy 179 IleLeuPheGlnPheTyrGln-----GlyHisThrGlyIleArgTyr 192
Db 372 -----TGAAGTTTCATGGCGCAGCAAGTCTCCAACTCTGGGATAGAGTGC 416
Qy 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCys 212
Db 417 ---GACTCTCAGGTACCTGCATCAACCCCTCTAATCTGGTGTGATGGCGGTGCACACTGC 473
Qy 213 LysLeuLysSerAspGluLeuGlyCysValArgPheAspTyrAspLysSerLeuLeuLys 232
Db 474 CCGCGCGGGAGGACGAGAAATCGGTGTGTTTGGCTCTACGACCAAACTTCATCTCTCAG 533
Qy 233 IleTyrSerGlySerSerHisGlnTyrLeuProIleCysSerSerAsnTyrAsnAspSer 252
Db 534 ATGTACTCATCTCAGAGGAAGTCTCTGCACCTGTGTGCCAAGACGACTGGAACGAGAAC 593
Qy 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluVal 272
Db 594 TACGGCGGGCGCGCTCGACGGACATCGGCTATAGAAATATATTTTACTCTAGCCAA--- 650
Qy 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db 651 GGAATAGTGGATGACGCGGATCCACGAGCTTTATGAACACTGAACACAGGCGCGGCAAT 710
Qy 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306
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Db      711  GTGATATCTATAAAACCTGTACACAGTGATGCTGTCTTCAAAGCAGTGGTTCT 770
QY      307  LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db      771  TTACGCTGTTAGCTCGGGGTCACACTCAAGCCGACAGCAGCATCGTGGGC 830
QY      324  GlyAlaLeuAlaSerAspSerLysTyrProTyrGlnValSerLeuHisPheGlyThr 343
Db      831  GGTGAGAGCGCGCTCCGGGGGCTGGCCCTGGCAGGTGAGCTGACGTCACGACGTC 890
QY      344  HisIleCysGlyGlyThrLeuIleAspAlaGlnTyrValLeuThrAlaAlaHisCysPhe 363
Db      891  CAGTGTGGAGGCTCCATCATCAACCCGAGTGGATCGTACAGCGCCCACTGGTG 950
QY      364  PheValThrArgGlnLysValLeuGly-----TyrLysValTyrAlaGlyThr 380
Db      951  -----GAAAAACCTCTTAAACATCCATGGCATTTGGACGGCAITTTGGGGATT 998
QY      381  SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db      999  TTGAGCAATCTTTTCATGTTCTATGGAGCGCGATACCAAGTACAAAAGTATTTCTCAT 1058
QY      399  SerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysPro 418
Db      1059  CCAATATTGACTCCAGACCAAGCAATGATGCTGCTGATGAGCTGCGAAGCCT 1118
QY      419  LeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db      1119  CTGACTTTCAACGACCTAGTGAACCAAGTGTGTCTGCCAACCCAGCGCATGTCTCGAG 1178
QY      439  LeuAsnGluThrCysThrPheThrGlyPheGlyThrArgGlnThrAspLysThr 458
Db      1179  CCGAAGACCTCTGCTGGATTTCCGGGTGGGGGCCACCGAGAG---AAAGGAAGACC 1235
QY      459  SerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyr 478
Db      1236  TCAGAAGTCTGAACCTGCAAGGTGCTTCTCATTTGAGACACAGATGCAACACAGA 1295
QY      479  LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGly 498
Db      1296  TATGCTATGACAAACCTGATCACACCGACCATGATCTGTGCGGCTTCTGCGAGGGAAC 1355
QY      499  ArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGlnAsnAsnArgTyr 518
Db      1356  GTGCTATCTTGCAGGTGACAGTGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1415
QY      519  TyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db      1416  TGGCTGATAGGGGATACAAAGCTGGGGTCTGGCTGTGCGCAAGCTTACAGACGAGGTG 1475
QY      539  TyrThrLysValThrGluValLeuProTyrPheTyrSerLysMetGluSer 555
Db      1476  TACGGGAATGTGATGTATTCACGGACTGGATTTATTCGACAAATGAAGCA 1526

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RESULT 5

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US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1

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Alignment Scores:

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Pred. No.:      2,19e-29      Length:      2413
Score:          727.50      Matches:      170
Percent Similarity: 49.70%      Conservative: 79
Best Local Similarity: 33.93%      Mismatches: 193
Query Match:      2,12e4      Indels:      59
DB:              3          Gaps:      13

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US-09-879-792-12 (1-562) x US-09-518-046-1 (1-2413)

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QY      107  ValThrThrSerProThrArgValTyrLeuValArgAlaThrProValGly----- 123
Db      30  GTAACACTGTGGCTACTATCTCTCCGTGGTGGCCATCTACATTTTGGGACTCGGGAAT 89
QY      124  ---AlaValProIleArgSerProAlaArgSerAlaPro-----AlaThrArgAla 140
Db      90  TATGAGTATAGGTGGAGGGGCGGATGTCAGAGGTCTCTGAATAGTACCATCGGG 149
QY      141  ThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArg----- 155
Db      150  GAAATGATCGCGCTCTGTGTGAAGCCCC---TTCTCATTCGATCGCTTTTGGCCTT 206
QY      155  ----- 155
Db      207  GATGATTGAAATAGTCTCTGTTCACACAGATGCATGCTGTCTGCACAGATCCTG 266
QY      156  -----GluGlyGlnLysGlnLeuProLeuIleGlyCysValLeuLeuLeu 170
Db      267  TCATCTGCTGCCATTGAAGTTTTTCCCAATCATCTCATTTGGGATCATTCGATTGATA 326
QY      171  IleAlaLeuValSerLeuIleLeuPheGlnPheTrpGlnGlyHisThrGlyIle 190
Db      327  TTAGCACTGCCATTTGGTCTGGGCATCCACTTCGACTGC-----TCAGGGAAG 374
QY      191  ArgTyrLysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValVal 210
Db      375  TACAGATGTCGTCTATCTCTTAAAGTGTATCGAGCTGATTAACATCGATGTACGAGTCTCG 434
QY      211  AspCysLysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeu 230
Db      435  GATTGCAAGACGCGGAGGACGAGTACCGCTGTGTCCGGTGGTGGTGGTGGTGGTGGTGG 494
QY      231  LeuLysIleTyrSerGlySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsn 250
Db      495  CTCAGGTGTTCCACAGCTGCTTCG-----TGAAGACCATGTGCTCCGATGACTGGAAG 548
QY      251  AspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThr 270
Db      549  GGTCTACTAGCAATGTTCCTCTGCCCACTGGGTTTCCCAAGCTATGTGATGTTCAGAT 608
QY      271  GluValAla-----HisArgAspPheAlaAsnSerPheSer 282
Db      609  AACCTCAGATGAGCTCGCTGGAGGGGAGTTCCGGGAGGAGCTTTGTGTCATCGATCAC 668
QY      283  IleLeuArgTyrAsn-----SerThrIleGlnGluSerLeuHis---ArgSerGluCys 299
Db      669  CTCCTGCCAGATGACACAGGTGACTCATACACCACTCAGTATATGTGAGGGGAGGTGT 728
QY      300  ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGly---LeuArgAlaMetThr 318
Db      729  GCCTCTGGCCAGTGGTTTACCTTGCAGTGCACAGCCTGTGTGTCATAGAAGGGGGCTACAGC 788
QY      319  GlyArgIleValGlyGlyValAlaLeuSerAspSerLysTrpProTyrGlnValSerLeu 338
Db      789  TCAGCATCGTGGGTGGAAACATGTCTCTCGCAGTGGCCCTGCGACGCCGACCTT 848
QY      339  HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThr 358

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Db 849 CAGTTCAGGGCTACACCTGCGGGGCTGTGTCATCAGCCCTGTGGATCATCAT 908
QY 359 AlaAlaHisCysPheValThrArgGluValLeuGluGlyTrpLysValTyrAla 378
Db 909 GCTGCACATGTGTATTGACTTG-----TACCTCCCAAGTCATGACCATCCAGG 962
QY 379 GlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu---IleIleIle 397
Db 963 GGTCTAGTTTCCTGTTGGCAATCCAGCCCATCCACTGTGTGGAGAGATTGCTAC 1022
QY 398 AsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLys 417
Db 1023 CACAGCAAGTACAAAGCCAAAGAGCTGGGCAATGACATGCCCTTATGAAGCTGGCGGG 1082
QY 418 ProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPhe 437
Db 1083 CCATCAGCTCAATGAATAATGATCCAGCCTGTGTGCTGCCCACTCTGAAGAGAACTTC 1142
QY 438 SerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspAspLys 457
Db 1143 CCCGATGAAAAGTGTCTGACGTCAAGATGGGGGCCACAGAGGATGGAGGTGAC--- 1199
QY 458 ThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAsp 477
Db 1200 GCCTCCCTCTGCTGAAACACAGCGGCGCTCCCTTGTATTCACCAAGATCTGCACACC 1259
QY 478 TyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGly 497
Db 1260 AGGACGTGTAGCGTGCATCATCTCCCTCCATGCTCTGCGGGGCTACCTGACGGGT 1319
QY 498 GlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArg 517
Db 1320 GCGGTGAACAGCTGCCAGGGGAGCAGCGGGGGGCGCTGGTGTGTCAAGAGAGGGCTG 1379
QY 518 TrpTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysProGly 537
Db 1380 TGGAGTTAGTGGAGGACAGCTTTGGCATCGCTGCCAGAGTGAACAGCTGGG 1439
QY 538 ValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSerGluVal 557
Db 1440 GTGTACACCGGTGTACCTCTCTGCTGACTGGATCCAGCAGCAGATGGAGAGACCTA 1499
QY 558 Arg 558
Db 1500 AAA 1502

RESULT 6

US-09-656-002-1
; Sequence 1, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
; FILE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/656,002
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-656-002-1

Alignment Scores:

Pred. No.: 1,04e-28 Length: 2079
Score: 713.00 Matches: 180
Percent Similarity: 48.08% Conservations: 83
Best Local Similarity: 32.91% Mismatches: 212
Query Match: 23.77% Indels: 74
DB: 4 Gaps: 15
US-09-879-792-12 (1-562) x US-09-656-002-1 (1-2079)
QY 42 AlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGlnAlaSerPro 61
Db 6 GCAGCAGCTTGTTCAGCGGACAGAGATCTGGGGGTGAGGACCAAGGCTCTGCCCT-GCA 64
QY 62 AlaGlyThrProGlyArgAlaSerProGlyArgAlaSer-----ProAlaGlnAla 79
Db 65 CTGGGGCTCTCTCCAGCCAGCTGACCCAGGAGCTTTCAGCTCTGCTGCCAGCAGGACC 124
QY 80 SerProAlaArgAlaSerProAlaLeu---AlaSerLeuSerArg-SerSerSerGlyAr 98
Db 125 TGTGTGGGGAGGCGCTCTCTGCTGCTGGGGGTGACAATCTCAGCTCCAGGCTCAGGGAG 184
QY 98 gSerSerSerAlaArgSerAlaSerValThrSerProThrArgValTyrLeuValAr 118
Db 185 ACCGGAGGATCAGCAGCCAGCATGTGTACAGGATCTCTG-ACAGTGATCAACCTCTGAAC 243
QY 118 gAlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaTh 138
Db 244 AGCTCTG-----ATGTCAAACCCCTCGCGCAAC----- 271
QY 138 rArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArgGluGlyGl 158
Db 272 -----CCCCATATCCCATGTGGAGACTTATCATATTGTGTGT 297
QY 158 nLys---GlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValSerLe 177
Db 298 AAGTGTGGGGTCTCCCATCATCATAGCCTTACAGCTTGGCGAGTATCATATTGTGTGT 357
QY 177 uIleIleLeu-----PheGlnPheTrpGlnGlyHisThrGlyIleAr 191
Db 358 TGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTCTCGCGGGCAG----- 406
QY 191 gTyrLysGluGlnArgGluSerCysProLysHisAlaVal-----ArgCysAs 207
Db 407 -----CCTCTCCACTTATCCCGAGGAGAGAGAGCTGTGTGA 441
QY 207 pGlyValValAspCysLysLeuLysSerAspGluLeuGlyCys----- 221
Db 442 CGGAGAGCTGGACTGTCTCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGA 501
QY 222 -----ValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGl 236
Db 502 AGGGCTCTGAGTGGCAGTCCGCTCTCCAAGACCGCATCCACACTGAGGTGTGACTC 561
QY 236 ySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsnAspSerTyrSerGly 256
Db 562 GGGCACAGGAGTGTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
QY 256 sThrCysGlnGlnLeuGlyPheGluSer-----AlaHisArgThrThrGluValAlaHi 274
Db 622 AGCCTGTAGGACAGTGGCTACAGCAGCAACCCACTTTCAGAGCTGTGGAGATTGGGCC 681
QY 274 sArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThrIleGlnGlnSerLe 294
Db 682 AGACCAGGATCTGGATGTTGTGAATAATCAGAAACACAGGAGGAGCTTCCAGTCGGAA 741
QY 294 uHisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLe 314
Db 742 CTCAGTGGGGCTGTCTCTCAGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 801
QY 314 uArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTr 334

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Db 802 GAGCCTGAACACCCCGTGTGGTGGGAGGAGCCCTCTGTGATTCCTGGCCCTTG 861
QY 334 pGlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAsePalaGl 354
Db 862 GCAGGTGAGCATCCAGTACACAAACAGCAGCAGTCTGTGGAGGAGCATCTCGACCCCA 921
QY 354 nTTPValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTr 374
Db 922 CTGGTCTCAGCGCAGCCCTGCTTC-----AGGAACATACCGATGTGTCAACTG 975
QY 374 pLysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGl 394
Db 976 GAAGGTGGCGGAGGCTCAGACAACTGGCGAGCTCCCATCCCTGGCT---GTGGCCAA 1032
QY 394 uIleIleIle-----AsnSerAsnTyrThrAspGluLysAspPyrAspIleAl 411
Db 1033 GATCATCATATGAAATTCACCCCATGTAC-----CCCAAGACAAATGACATCGC 1083
QY 411 aLeuMetArgLeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuPr 431
Db 1084 CCTCATGAGCTGAGTCCCACTCACTTCTCAGGCACAGTCAGGCCCATCTGTCTGCC 1143
QY 431 oMetHisGlnThrPheSerLeuAsnGluThrCysfTrpIleThrGlyPheGlyLysTh 451
Db 1144 CTTCCTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGCTTAC 1203
QY 451 rArgGluThrAspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAs 471
Db 1204 GAAGCAGAAATGGAGGAAGATGTCTGACACTGCTGCAGGCGTCAGTCAGGCTATTGA 1263
QY 471 pPheLysLysCysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCy 491
Db 1264 CAGCACACGGTGCATTCAGACAGCATCGTACACAGGGGGAGTCCACGAGAGATGATGT 1323
QY 491 sAlaGlyAspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuVa 511
Db 1324 TGCAGGCATCCCGAAGGGGGTGTGGACACCTCCAGGGTGACAGTGGTGGGCCCTGAT 1383
QY 511 lCysGluGlnAsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGl 531
Db 1384 G---TACCATCTGACCGAGGCGATGTGTGGGCGATCGTTAGCTGGGGCTATGGCTGCGG 1440
QY 531 yGlnArgAsnLysProGlyValTyrThrLysValThrLysValLeuProTyrTrpIleTyrSe 551
Db 1441 GGCGCCGAGCACCCAGGAGTATACACCAAGTCTCAGCCTATCTCACTGGATCTACAA 1500
QY 551 rLysMetGluSerGluVal 557
Db 1501 TGTCTGGAAGGCTGAGCTG 1519
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RESULT 7

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US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6234663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3
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Alignment Scores:

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Pred. No.: 2,36e-28 Length: 2544
Score: 708.00 Matches: 175
Percent Similarity: 46.78% Conservative: 79
Best Local Similarity: 32.23% Mismatches: 190
Query Match: 23.61% Indels: 100
DB: 3 Gaps: 15
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US-09-879-792-12 (1-562) x US-09-518-046-3 (1-2544)

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QY 107 valThrThrSerProThrArgValTyrLeuValArgAlaThrProValGly----- 123
Db 30 GTAACACTGTGGCTACTATCTCTCCGTGGTGCCTACATTTTGGGACTCGGGAAAT 89
QY 124 ---AlaValProIleArgSerProAlaArgSerAlaPro-----AlaThrArgAla 140
Db 90 TATGAGTAGAGTGGGCGGAGCCGGATGTGCAGAGTCTCTCAATAGTACCATCGGG 149
QY 141 ThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArg----- 155
Db 150 GAAATGATCGGCTCTGTGTGAAGCCCG---TTCATTCGATCGCTTTTGGGCTT 206
QY 155 ----- 155
Db 207 GATGATTGAAATAAGTCTCTGTGCACAGATGCAGATGCTGTGTCACAGATCTCTG 266
QY 156 -----GluGlyGlnLysGlnLeuProLeuIleGlyCysValLeuLeuLeu 170
Db 267 TCACCTCTGCCATTGAGTGTTCCTCAATCATCTCATTTGGGAGTCAATGATGATA 326
QY 171 IleAlaLeuValSerLeuIleLeuPheGlnPheTrpGlnGlyHisThrGlyIle 190
Db 327 TTAGCATTGGCATTGGTCTGGGCATCCACTTCGACTGC-----TCAGGGAAG 374
QY 191 ArgTyrLysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValVal 210
Db 375 TACAGATGCTGCTATCTTTAAGTGTATCGAGCTGATTAATCGATGTGACGGAGTCTCG 434
QY 211 AspCysLysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeu 230
Db 435 GATTGCAAGAGCGGGAGGAGCAGATACCCCTGTGTCGGTGGTGGTGGTGGTGGTGG 494
QY 231 LeuLysIleTyrSerGlySerHisGlnTrpLeuProIleCysSerSerAsnTrpAsn 250
Db 495 CTCAGGTGTTACAGCTGCTTCG-----TGAAGACCATGTGCTCCGATGCTGAAG 548
QY 251 AspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThr 270
Db 549 GGTCTACTAGCAAAATGTTGCTGTCGTCACCACTGGGTTTCCCAAGCTATGTAAAGTTC 608
QY 271 GluValAla-----HisArgAspPheAlaAsnSerPheSer 282
Db 609 AACCTCAGAGTGTGCTGCGAGGGCGAGTTCGGGAGGAGTGTGTGTCATCGATCAC 668
QY 283 IleLeuArgTyrAsn-----SerThrIleGlnGlnSerLeuHis---ArgSerGluCys 299
Db 669 CTCCTTGGCAGATGACAGGTGACTGCATTTACACCACTCAGTATATGTGAGGAGGATGT 728
QY 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGly---LeuArgAlaMetThr 318
Db 729 GCCTCTGGCCAGCTGTACCTTGCAGTGCACAGCCTGTGGTGCATAGAGGGGCTACAGC 788
QY 319 GlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTyrGlnValSerLeu 338
Db 789 TCACCATCTGTGGTGGAAACATGCTCTGCTCTGCGAGTGGCCCTTGGCAGGCCACCTT 848
QY 339 HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThr 358
Db 849 CAGTTCCAGGGCTACCACTGTGGGGGGCTCTGTGTCATCACGCCCTCTGTGATCATCAT 908
QY 359 AlaAlaHisCysPhePhe-----ValThrArgGluLysVal----- 370
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Db 909 GCTGCACACTGTGTTATGAGTTTCTAGTCTCTAGAGAAAGGGCAGACAGAGAGAGG 968
Qy 371 -----LeuGlugly-----
Db 969 AAGCTCCTGTGTGTGAGGAAACCCACAAAATGAAGGACCTAGACCTTCCCATAGCTAA 1028
Qy 374 -----TyrLysValTyrAlaGlyThrSerAsnLeuHisGln----- 385
Db 1029 TTCAGTGCACCATGTTATGAGATAGACAGAGCTGTACTCTCCCAAGTCATGGACCATCC 1088
Qy 386 -----LeuProGluAlaAlaSerLeuAlaGluLeu 395
Db 1089 AGGTGGGTCTAGTTTCCCTGTGTGACAAATCCAGGCCCATCCCACTTG-GTGGAGAGATT 1147
Qy 396 llelleAsnSerAsnTyrThrAspGluGluAspTyrAspIleAlaLeuMetArgLeu 415
Db 1148 GTCTACCAACAGAGTACAGCAAGGAGGCTGGGCAATGATCGCCCTTATGAGCTG 1207
Qy 416 SerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGln 435
Db 1208 GCCGGGCCCATCTCAGCTTCAATGAATGATCCAGCCTGTGTGCTGCCCACTCTGAAGAG 1267
Qy 436 ThrPheSerLeuAsnGluThrCysTyrIleThrGlyPheGlyLysThrArgGluThrAsp 455
Db 1268 AACTTCCCCGATGGAAAGTGTGCTGGAGCTCAGGATGGGGGGCCACAGAGATGAGGT 1327
Qy 456 AspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCys 475
Db 1328 GAC---GCCTCCCTGTCTGTAACACAGCGGGCGCTCTTGTGTTTCCACAGATCTGC 1384
Qy 476 AsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeu 495
Db 1385 AACCAACAGGAGCTGTACGGTGGCATCATCTCCCTCCCTCCAGCTCTGCGCGGCTACCTG 1444
Qy 496 ArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsn 515
Db 1445 ACGGTGGGTGGAGCAGCTGCCAGGGGACAGCGGGGGGCCCTCTGTGTGTCAAGAGAG 1504
Qy 516 AsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsnLys 535
Db 1505 AGCGTGTGGAAGTTAGTGGGAGCAGCAGCTTTGGCATCGGCTGGCGAGAGGTGAACAAG 1564
Qy 536 ProGlyValTyrThrLysValThrGluValLeuProTyrIleTyrSerLysMetGluSer 555
Db 1565 CTGGGGTGTATACCGGTGTACCTCTCTCTGGACTGATCCACGAGCAGATGAGAGA 1624
Qy 556 GluValArg 558
Db 1625 GACCTAAA 1633

```

RESULT 8

US-09-008-271A-18
 ; Sequence 18, Application US/09008271A
 ; Patent No. 6203979
 ; GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 Hillman, Jennifer L.
 Yue, Henry

Guegler, Karl J.
 Corley, Neil C.
 Tang, Tom Y.
 Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSES: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008, 271A

FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mohan-Peterson, Sheela

REGISTRATION NUMBER: 41,201

REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 2038 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: COLN0713

CLONE: 1337018

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-008-271A-18

Alignment Scores:
 Pred. No.: 1,966-28 Length: 2038
 Score: 707.50 Matches: 176
 Percent Similarity: 47.43% Conservative: 82
 Best Local Similarity: 32.35% Mismatches: 214
 Query Match: 23.59% Indels: 73
 DB: 3 Gaps: 14

US-09-879-792-12 (1-562) x US-09-008-271A-18 (1-2038)

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Qy 44 AlaSerProAlaGlyThrProGlyArgAlaSerProAlaGlnAlaSerProAlaGly 63
Db 4 GCTTGCTCAGCGGACAGGATGCTGGCGGTGAGGACCAAGGCTGCCTT-GCACTCGGG 62
C/ 64 ThrProGlyArgAlaSerProGlyArgAlaSer-----ProAlaGlnAlaSerPro 81
Db 63 CTCTCTCAGCCAGTGTCTGACCGAGGACTTCTGACCTCTGGCCAGCCAGGACCTGTGTG 122
Qy 82 AlaArgAlaSerProAlaLeuAlaSerLeuSerArgSerSerSerGlyArgSerSer 101
Db 123 GGGAGGCGCTCTGCTGCCTT---GGGGTGACAATCTCAGCTCCAGGCTACAGGAGACC 179
Qy 102 AlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArgAlaThr 121
Db 180 GGGAGGATCAGAGCCAGCATGATCTCTGACAGTATCACTTCACTGAAACAGGCTCG--- 236
Qy 122 ValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThrArgAlaThr 141
Db 237 -----ATGTCAACCCCTGCGCAAC----- 257
Qy 142 ArgGluSerProGlyThrSerLeuProLysPheThrTrpArgGluGlyGlnLys--GlnL 161
Db 258 -----CCGTATCCCATGAGAGACCTTCAGAAAGTGGGGA 293
Qy 161 euProLeuIleGlyCysValLeuLeuIleAlaLeuValSerLeuIleLeu-- 180
Db 294 TCCCATCATCATAGACACTACTGAGCTGGCGGATATCATCATGTGTGTCTCTATCA 353
Qy 181 -----PheGlnPheTrpGlnGlyHisThrGlyIleArgTyrLysGlu 195
Db 354 AGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAG----- 391
Qy 195 lnArgLysCysProLysHisAlaVal-----ArgCysAspGlyValVala 211
Db 392 -----CCTCTCCACTTCTATCCGAGGAGCAGCTGTGTGACGGAGAGCTGG 437

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Db 549 GGTCACTACGAAATGTTGCTGTCGCAACTGGGTTTCCCAAGCTATGTGAGTTCAGAT 608
Qy 271 GluValAla-----HisArgAspPheAlaAsnSerPheSer 282
Db 609 AACCTCAGATGAGCTGCTGGAGGGGCGAGTTCGCGGAGGAGTTCGTCCTCAGATCAC 668
Qy 283 IleuArgTyrAsn-----SerThrIleGlnLeuSerHis---ArgSerGluCys 299
Db 669 CTCTTGCAGATGACAAAGGAGTGCATATACCACTCAGTATATGTGAGGAGGAGTGT 728
Qy 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGly---LeuArgAlaMetThr 318
Db 729 GCCTCTGGCCACGCTGTGTTACTCTTCAGTGCACAGCTCTGTCATAGAGGGGCTACAGC 788
Qy 319 GlyArgIleValGlyGlyAlaLeuAlaSerAspSerIleTyrProThrGlnValSerLeu 338
Db 789 TCACGCATCTGCTGGTGAACATGCTCTCTCTCGCAGTGGCCCTGGCAGGCGCAGCTT 848
Qy 339 HisPheGlyThrThrHisIleCysGlyGlyGlyThrLeuIleAspAlaGlnTyrValLeuThr 358
Db 849 CAGTTCAGGGCTACCACTCTGTCGGGGGCTCTGTCATCAGCCCTCTGGATCATCAT 908
Qy 359 AlalaHisCysPhePheValThrArgGluValLeuGluGlyTyrPylsValTyrAla 378
Db 909 GCTGCACACTGTGTTATGACTTG-----TACCTCCCAAGTGCATGACCATCCAGGTG 962
Qy 379 GlyThrSerAsnLeuHisGlnLeuProGluAlaSerIleAlaGlu---IleIleIle 397
Db 963 GGTCTAGTCTCCCTGTTGGACATCCAGCCCATCCCACTGTGTGGAGAGATGTTTAC 1022
Qy 398 AsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerIle 417
Db 1023 CACAGCAAGTACAGCCCAAGAGGCTGGGCAATGACATCGCCCTTATGAAGTGGCGGG 1082
Qy 418 ProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPhe 437
Db 1083 CCATCAGCTTCAGAAATGATCCAGCTGTGTGCTGCTGCCAATCTGAGAGACTTC 1142
Qy 438 SerLeuAsnGlnThrCysIleThrGlyPheGlyThrArgGluThrAspAspLys 457
Db 1143 CCCGATGGAAAGTGTCTGCAGCTCAGGATGGGGGCCACAGAGGATGGAGTGAC--- 1199
Qy 458 ThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheValLys---CysAsnAs 477
Db 1200 GCCTCCCTGCTCCGTAACAGCGCGCGCTGCTCTTGATTTCCAAAGATCTGCACCA 1259
Qy 477 pTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlu 497
Db 1260 CAGGACGCTGTACGCTGCATCATCTCCCTCCATGCTCTGCGGGCTTACCTGACGGG 1319
Qy 497 yGly--ArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGlnAsnAsn 516
Db 1320 TGGCGTTGGAACAGCTGCAGGGGAGCAGCGGGGGCCCTGTGTGTCTCAAGAGAGGAGG 1379
Qy 517 ArgTyrPyrLeuAlaGlyValThrSerTyrPylsThrGlyCysGlyGlnArgAsnLysPro 536
Db 1380 CTGTGGAGATGTAGTGGAGGACACAGCTTTGGCATCGCTGGCAGAGCGTGAACAGCT 1439
Qy 537 GlyValTyrThrLysValThrGluValLeuProTyrPylsThrSerLysMetGluSerGlu 556
Db 1440 GGGGTGTACACCGGTGTACCTCTCTGACTGGATCCACGAGCAGATGGAGAGAGAC 1499
Qy 557 ValArg 558
Db 1500 CTAAAA 1505

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RESULT 10
 US-09-742-703-3
 ; Sequence 3, Application US/09742703
 ; Patent No. 6423543
 ; GENERAL INFORMATION:
 ; APPLICANT: Patrick Allen Marcotte

APPLICANT: Lex M. Cowsett
 TITLE OF INVENTION: ANTISENSE MODULATION OF HEPsin EXPRESSION
 FILE REFERENCE: KIS-0090
 CURRENT APPLICATION NUMBER: US/09/742,703
 CURRENT FILING DATE: 2000-12-20
 NUMBER OF SEQ ID NOS: 49
 SEQ ID NO 3
 LENGTH: 2363
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (826)..(2079)
 US-09-742-703-3

Alignment Scores:
 Pred. No.: 3,21e-26 Length: 2363
 Score: 666.00 Matches: 199
 Percent Similarity: 45.53% Conservative: 86
 Best Local Similarity: 31.79% Mismatches: 218
 Query Match: 22.21% Indels: 124
 DB: 4 Gaps: 24

US-09-879-792-12 (1-562) x US-09-742-703-3 (1-2363)

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Qy 6 HisGlyAsnAlaSerProAla-----ArgThrProSerAlaGlyAla 19
Db 312 CACTATGAGCTCTCCCAAGCAGCCTAGGTGTCTGCTCTCTCTCTCTCAGACTCAGCC 371
Qy 20 SerProAlaGlnAlaSerProAlaGlyThr-----ProGlyArgAlaSer 35
Db 372 GTTGGACCCAGTCTCTTCTCTCCAGACCCAGAGTTCAGCCCTCAGCCCTCTCTCC 431
Qy 36 ProAlaGlnAlaSerProAlaGln-----AlaSer 45
Db 432 CTCATCTAGGAGTCTCTGGCCCCCAATTCCTCTTCCCAAGACTTATGATTTCAAGT 491
Qy 46 ProAlaGlyThrProGlyArgAlaSerProAlaGlnAlaSerProAlaGlyThrPro 65
Db 492 CCTCAGCTGTCTCTCTCTCTCAACCCGGGATCT-----CAGTCCCTCTCTCT 539
Qy 66 ProGlyArgAlaSerProGlyArgAlaSerProAlaGlnAlaSerProAlaArgAlaSer 85
Db 540 CCAGGC-----TCAGGATGGGGTCCCATCTCCCAATCCAGG-CGTCCCCC 589
Qy 86 ProAlaLeuAlaSerLeuSerArgSerSerSerSerSerSerSerAlaArgSerAla 105
Db 590 GCTGCTGTCTCAGACACTGACCCCATCC-----TTGACCCAGCCCAATCTGCG 637
Qy 106 SerValThrThrSer-----ProThrArgValTyrLeuValArg 118
Db 638 TCCGTGATCAGCGGTGTCTGCGCCAGGCCAGTCTCTACAGCTCTGCTGGATGGAGCG 697
Qy 119 -----AlaThrProValGly-----AlaValProIleArg 128
Db 698 CTGGAGCTGGGGGGCCAGGACTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 757
Qy 129 SerSerProAlaArgSerAlaProAla--ThrArgAlaThrArgGluSer-----ProG 146
Db 758 CCACTCTCTCAGACTCCACCTCTGGCCAGAGAGTTCAGCCAGGAGTATCATTAACAGAG 817
Qy 146 lYThrSerLeuProLysPheThrTyrArgGluGlyGlnLysGlnLeuPro----- 162
Db 818 GCAGTGACATGGCGCAG-----AAGGAGGGTGGCGAGCTGCTGCTGCTGCTGCTGCTCA 868
Qy 163 -----LeuIleGlyCysValLeuLeuLeuLeuValValVal 176
Db 869 GACCAAGGTGGAGCTCTCTCTCGGGGAGCCCTCTGCTACTTCTGACAGCCATCGGGCGG 928
Qy 176 eLeuIleIleLeuPheGlnPheThrGlnGlyHisThrGlyIleArgTyrLysGlnAla 196
Db 929 CA-----TCCTGG----- 936

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196 rgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCysLysLeuLys 216
937 -----GCAATGTGGCTGTCTCTCCTCAGGA 961
216 erAspGlu-----LeuGlyCysValArgPheAspTrpAspLysSerLeuLeuLysIle 234
962 GTGACAGGAGCCGCTGTACCCAGTGAGGTGAGCTCTGGGAGCGCTCGCTCATGTCT 1021
234 yrSerGlySerSerHisGlnTrpLeuProLysCysSerSerAsnTrpAsnAspSerTrs 254
1022 TTGACAAGAGGAGGAGGAGCGCTGGCGCTGTCTCTCGCTCCCAACGCGAGGAGTAG 1081
254 erGluLysTrpCysGlnGlnLeuGlyPheGluSerAlaHisArgTrpThrGluValAlah 274
1082 CCGACTCAGCTGCGAGGAGATGGCTTCTCAGGAGCTGACCCACTCCGAGCTGAGCG 1141
274 isArgAsp-----PheAlaAsnSerPheSerIleLeuA 285
1142 TGGCAAGCGCGGCGCAATGGCAGCTCGGCGTCTTCTGTGTGGAGGAGGAGGTGC 1201
285 rgTyrAsnSerThrIleGlnGluSerLeuHisArgSerGluCysProSerGlnArgTyrI 305
1202 CCCACACCGAGGCTGTGAGGTGATCTCCCGTGTGTGATGCCCCAGAGCGGTTCT 1261
305 leSerLeuGlnCysSerHisCysGlyLeuArgAlaMet---ThrGlyArgIleValGlyG 324
1262 TGGCGCGCATCTGCCAGACTGTGGCGGAGAGTCCCGTGGAGCGCATCGTGGGAG 1321
324 lyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHisPheGlyThrThr 344
1322 GCGGGGACACCGACTGTGGCGGCGGTGGCGTGGAGTCCGTTGATGATGAGGACAC 1381
344 isIleCysGlyGlyThrLeuLeuAspAlaGlnTrpValLeuThrAlaAlaHisCysPheP 364
1382 ACCCTGTGGGGGATCCCTGCTCCCGGGAGTGGTGTGTGATGCCCCAGAGCGGTTCT 1438
364 heValThrArgGluLysValLeuGluGlyTrpLysValTrAlaGlyThr-----S 381
1439 TCCCGAGCGAACCGGGTCTGTCCCGATGCGGAGTGTTCGCGGTGGCGTGGCCGAG 1498
381 erAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleAsnSerAsn 401
1499 CCTCTCCCGACGGTCTG-----CAGCTGGGGGTGAGGCTGTGGTCTACCGGGGGCT 1552
401 yr-----ThrAspGluGluAspAspTyrAspIleAlaLeuMetArgL 415
1553 ATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAGACAGCATATTCCTGTCACCC 1612
415 euSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyG 435
1613 TCTCAGTCCCTGCTCCCTCAGAGATACATCCAGCTGTGTGCTCCAGCTCCCGGCC 1672
435 inThrPheSerLeuAsnGluThrCysTrpIleLeuGlyPheGlyLysThrArgGluThrA 455
1673 AGGCCTGTGTGATGGCAAGATCTGTACCGTGAGCGGTGGGCAACAGCATGATGTCT 1732
455 spAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysysc 475
1733 GCCAACAGCGCGGG---GTACTCCAGGAGGCTCGAGTCCCATATATGAGCATGATGTCT 1789
475 ysAsnAspTyrIleuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspL 495
1790 GCAATGGCGCTGACTTCTATGGAACACCATGATCAAGCCCAAGATGTCTGTGCTGGCTACC 1849
495 euArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGlu----- 513
1850 CCGAGGGGTGGATTCATGCTCCAGGAGGAGGAGCGGTGGTCCCTTGTGTGAGGACA 1909
514 -----GlnAsnAsnArgTrpTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysG 531
1910 GCATCTCTCGGAGCGGCGGCTGTGGCGCTGTGGCATGTGTGGGCGACTGGCTGTG 1969
531 lyGlnArgAsnLysProGlyValTyrThrLysValThrGluValLeuProTrpIleTyrS 551

1970 CCTGGCCCGAGGAGCGCTCTACACCAAGTCAAGTCAAGTCTCGGAGTGGATCTTCC 2029
551 erLysMetGluSer 555
2030 AGGCCATAAAGACT 2043
RESULT 11
US-09-510-738A-188
; Sequence 188, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length cDNA of hepsin
US-09-510-738A-188
Alignment Scores:
Pred. No.: 3,848-25 Length: 1783
Score: 642.50 Matches: 170
Percent Similarity: 46.01% Conservative: 78
Best Local Similarity: 31.54% Mismatches: 203
Query Match: 21.42% Indels: 89
DB: 3 Gaps: 17
US-09-879-792-12 (1-562) x US-09-510-738A-188 (1-1783)
QY 54 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProGlyArg 73
DB 1 TCGAGCCGCTTTCAGGAGCCCTACCTGAGGCGCCACAGGTGAGGCA-----48
QY 74 AlaSerProAlaGlnAlaSerProAlaGlyThrProAlaGlyThrProAlaGlyThr 93
DB 49 -----GCTGGCTAGCAGGCCCCAC---GCCACGCTCTGCTCTCCAG 90
QY 94 SerSerSerGlyArgSerSerSerAlaArgSerAlaSerValThrThrSerProThrArg 113
DB 91 CCGCCCGCTGCTCGGGGCGCCACCATGCTCTGCTCCAGGCTGAGACTGACCCGACC---147
QY 114 ValTyrLeuValArgAlaThrProValGlyAlaValProIleArgSerSerProAlaArg 133
DB 148 -----CCGCACTACTCGAGCTCCGCCCCACCTGCTGAGCCCCAGGGTCC 195
QY 134 SerAlaProAlaThrArgAlaThrArgGluSer-----ProGlyThrSerLeuProLys 151
DB 196 CACCTCTGG---CCAGGAGGTACCCAGGAGATCATTAACAGAGGAGGAGTGCATGCGGAG 254
QY 152 PheThrTrpArgGluGlyGlnLysGlnLeuPro-----162
DB 255 -----AAGAGGGTGGCGGAGTGTGCTGCTCCAGACCCCAAGGTGGCAGCT 305
QY 163 ---LeuIleGlyCysValLeuLeuLeuIleAlaLeuValSerLeuIleIleLeuPhe 181
DB 306 CTCACCTGGGAGCCCTGCTACTTCTGACAGCCATTCGGGGCGGCA-----350
QY 182 GlnPheTrpGlnGlyHisThrGlyIleArgTyrLysGluGlnArgLysSerCysProLys 201
DB 351 ---TCCTGG-----356
QY 202 HisAlaValArgCysAspGlyValValAspCysLysLysLeuLysSerAspGlu-----Leu 219

ORGANISM: HUMAN
US-09-820-002-1

Alignment Scores:

Pred. No.: 1.29e-23 Length: 1615
Score: 612.00 Matches: 154
Percent Similarity: 45.40% Conservative: 68
Best Local Similarity: 31.49% Mismatches: 169
Query Match: 20.41% Indels: 98
DB: 4 Gaps: 16

US-09-879-792-12 (1-562) x US-09-820-002-1 (1-1615)

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QY 95 SerSerGlyArgSerSerSerAlaArgSerValThrThrSerProThrArgVal 114
Db 16 TCACACGGGAGGAGAACAGCCCTGTCA-----ACTGTGGCCCGGGAACTG 66
QY 115 TyrLeuValArgAlaThrProValGlyAlaVal-----ProIleArgSerSerProAla 132
Db 67 GGCCTGGGGAGG---ACATGCTTGGGCAATAAAGTTAGCCCTGGGGGCGAGGAGCT 123
QY 133 ArgSerAlaProAlaThrArgAlaThrArgGluSerProGlyThrSerLeuProLysPhe 152
Db 124 GGCCTGGGGCCAGACCCCTGGCGCAATGAGGACAGGCTTGGCTGTGGC---CCAGCATG 180
QY 153 ThrTrpArgGluGlyGlnLysGlnLeuPro-----162
Db 181 GTGCTGTGTGAGGTGGCGGAGCTGTGCCATGCTGCCAGACCACCAAGGTGGCAGCTCTC 240
QY 163 LeuIleGlyCysValLeuLeuLeuLeuAlaLeuValSerLeuIleLeuPheGln 182
Db 241 ACTGGGGAGCCCTGTCTACTTCTGACAGCCATCGGGGGCGGCA-----282
QY 183 PheTrpGlnGlyHisThrGlyIleArgTyrLysGluGlnArgGluSerCysProLysHis 202
Db 283 TCCTGG-----288
QY 203 AlaValArgCysAspGlyValValAspCysLysLysLeuLysSerAspGlu-----LeuGly 220
Db 289 -----GCCATTGTGGCTGTCTCTCTCAGGAGTGACCGAGGCGCGCTGTAC 333
QY 221 CysValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGlySerSerHisGln 240
Db 334 CCAAGTCAGTCAGCTCTGGGAGCGCTCGGCTCATGCTTTTGACAGAGGAGGAGGAG 393
QY 241 TrpLeuProIleCysSerSerAsnTrpAsnAspSerTyrSerGluLysThrCysGlnGln 260
Db 394 TGGCGGCTGCTGTGCTCTCTCGGCTCCAAACGCCAGGCTAGCCGAGCTCAGCTGCGAGGAG 453
QY 261 LeuGlyPheGluSerAlaHisArgThrGluValAlaHisArgAspPheAlaHisSer 280
Db 454 ATGGGCTTC-----462
QY 281 PheSerIleLeuArgTyrAsnSerThrIleGlnGluSerLeuHisArgSerGluCysPro 300
Db 463 -----CTCAGTCATTGCCCC 477
QY 301 SerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMet---ThrGly 319
Db 478 AGAGGCGGTTCCTGGCCCGCATCTCCAGACTGTGGCCGAGGAGTGGCCGCTGGAC 537
QY 320 ArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHis 339
Db 538 CGCATCTGGGAGGCGGGGACACAGCTTGGGCGGTGGCCCTGGCAAGTCAGCTTGGC 597
QY 340 PheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThrAla 359
Db 598 TATGATGAGACACACTCTGTGGGGATCCCTCTCTCCGGGAGCTGGGTGTGACAGCC 657
QY 360 AlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAlaGly 379
Db 658 GCCCACTGC---TTCCCGGAGCGGAGACCGGGTCTCTGTCGGATGGCGAGTGTTCGGGT 714
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QY 380 Thr-----SerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIle 396
Db 715 GCGTGGCCAGGCGCTCTCCCAAGGCTCTG-----CAGCTGGGGTGGAGGTGGTCTC 768
QY 397 IleAsnSerAsnTyr-----ThrAspGluGluAspAspTyrAspIle 410
Db 769 TACCACGGGGGCTATCTTCCCTTTCCGGGACCCCAACAGAGGAGGAGAACAGCATATT 828
QY 411 AlaLeuMetArgLeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeu 430
Db 829 GGCCTGGTCCACTCTCCAGTCCCTCCCTCCAGTAATACATCCAGCTGTGTGCTCTC 888
QY 431 ProMetHisGlyGlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLys 450
Db 889 CCAGCTCCGGCCAGGCGCTGGTGGATGCAAGATCTGTACCGTACCGGCTGGGGCAAC 948
QY 451 ThrArgGluThrAspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIle 470
Db 949 ACAGCATCTATATGCGCAACAGGCGCGG---GTACTCCAGAGGCTCGAGTCCCATATC 1005
QY 471 AspPheLysLysCysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMet 490
Db 1006 AGCATGATCTCTGCATGCGCTGACTTCTATGGAACCCAGATCAAGCCCAAGATGTC 1065
QY 491 CysAlaGlyAspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeu 510
Db 1066 TGTGCTGCTACCCCGAGGCTGGCATTTGATCCCTGCCAGGCGGACAGCGGTGTCTCTT 1125
QY 511 ValCysGlu-----GlnAsnAsnArgTyrTyrLeuAlaGlyValThrSerTrp 526
Db 1126 GTGTGTGAGGACAGCATCTCTCGACCGCACGTTGGCGCTGTGTGCGCATTTGAGTGG 1185
QY 527 GlyThrGlyCysGlyGlnArgAsnLysProGlyValTyrThrLysValThrGluValLeu 546
Db 1186 GGCATGGCTGTGCTCGCTGGCCAGAGCCAGAGGCTCTACACCAAGTCACTGACTTCCCG 1245
QY 547 ProTrpIleTyrSerLysMetGluSer 555
Db 1246 GAGTGGATCTTCCAGGCCATAAAGACT 1272
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Search completed: December 17, 2003, 21:55:35
Job time : 138 secs